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(54) Title: METHOD FOR PURIFYING KERATINOCYTE GROWTH FACTORS		
(57) Abstract		
The present invention concerns the purification of keratinocyte growth factors.		

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METHOD FOR PURIFYING KERATINOCYTE GROWTH FACTORS

Field of the Invention

5 The present invention relates to the field of protein purification. Specifically, the present invention relates to the field of purifying keratinocyte growth factors.

10 Background of the Invention

 Polypeptide growth factors are important mediators of intercellular communication (Rubin et al. (1989), *Proc. Natl. Acad. Sci. USA*, 86:802-806). These
15 molecules are generally released by one cell type and act to influence proliferation of other cell types.

 One family of growth factors is the fibroblast growth factors (FGF). There are currently eight known FGF family members which share a relatedness among
20 primary structures: basic fibroblast growth factor, bFGF (Abraham et al. (1986), *EMBO J.*, 5:2523-2528); acidic fibroblast growth factor, aFGF (Jaye et al. (1986), *Science*, 233:541-545); int-2 gene product, int-2 (Dickson & Peters (1987), *Nature*, 326:833); hst/kFGF
25 (Delli-Bovi et al. (1987), *Cell*, 50:729-737, and Yoshida et al. (1987), *Proc. Natl. Acad. Sci. USA*, 84:7305-7309); FGF-5 (Zhan et al. (1988), *Mol. Cell. Biol.*, 8:3487-3495); FGF-6 (Marics et al. (1989), *Oncogene*, 4:335-340); keratinocyte growth factor (Finch
30 et al. (1989), *Science*, 24:752-755; Rubin et al. (1989), *Proc. Natl. Acad. Sci. USA*, 86:802-806; Ron et al. (1993), *The Journal of Biological Chemistry*, 268(4):2984-2988; and Yan et al. (1991), *In Vitro Cell. Dev. Biol.*, 27A:437-438); and hisactophilin (Habazzettl
35 et al. (1992), *Nature*, 359:855-858).

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Among the FGF family of proteins, keratinocyte growth factor (KGF) is a unique effector of non-fibroblast epithelial (particularly keratinocyte) cell proliferation derived from mesenchymal tissues. The term "native KGF" refers to a natural human (hKGF) or recombinant (rKGF) polypeptide (with or without a signal sequence) as depicted by the amino acid sequence presented in SEQ ID NO:2 or an allelic variant thereof. [Unless otherwise indicated, amino acid numbering for molecules described herein shall correspond to that presented for the mature form of the native molecule (i.e., minus the signal sequence), as depicted by amino acids 32 to 194 of SEQ ID NO:2.]

Native KGF may be isolated from natural sources. For example, hKGF can be isolated from medium conditioned by an embryonic lung fibroblast cell line (Rubin et al. (1989), *supra*. Three chromatographic steps, namely heparin-Sepharose™ (Pharmacia, Piscataway, NJ) affinity chromatography, HPLC gel filtration, and reverse-phase HPLC, were used to obtain a purified hKGF preparation. Approximately 6 mg of hKGF were recovered from 10 liters of conditioned medium. These chromatographic steps only recovered 0.8% total hKGF based upon a mitogenic activity assay. A further example teaches the use of another chromatographic step using heparin-Sepharose™ affinity and Mono-S™ ion-exchange chromatographys (Pharmacia, Piscataway, NJ) for isolation of rKGF produced in bacteria (Ron et al. (1993), *Journal of Biological Chemistry*, 268:2984-2988).

The properties of keratinocyte growth factors suggest a potential for the application thereof as a drug for promoting specific stimulation of epithelial cell growth. It therefore would be desirable to develop a method or methods for obtaining relatively high levels of homogeneous keratinocyte growth factors to provide sufficient quantities of material for comprehensive in

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vitro and in vivo biological evaluation and for a potential therapeutic application.

It is the object of this invention to provide a novel method for the purification of keratinocyte growth factors.

Summary of the Invention

The present invention is directed to a first method for purifying a keratinocyte growth factor (KGF), the method comprising:

- a) obtaining a solution containing KGF;
- b) binding KGF from the solution of part (a) to a cation exchange resin;
- 15 c) eluting KGF in an eluate solution from the cation exchange resin;
- d) passing the eluate solution from part (c) through a molecular weight exclusion matrix; and
- 20 e) recovering KGF from the molecular weight exclusion matrix.

The invention is further directed to a second method for purifying a keratinocyte growth factor (KGF), the method comprising:

- a) obtaining a solution containing KGF;
- b) binding KGF from the solution of part (a) to a cation exchange resin;
- 30 c) eluting KGF in an eluate solution from the cation exchange resin;
- d) performing hydrophobic interaction chromatography on the eluate solution of part (c); and
- 35 e) recovering KGF from the hydrophobic interaction chromatography step of part (d).

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Generally, the cation exchange chromatography step of the first or second methods may be conducted with any suitable buffer (e.g., phosphate buffer saline, sodium acetate or tris-HCL) at a pH of preferably
5 between about 6.8-7.5. Suitable columns for use in this step include carboxymethyl cellulose, carboxymethyl agarose and sulfated agarose and cellulose columns (e.g., columns of S-Sepharose Fast Flow™ resin, Mono-S™ resin and CM-cellulose™ resin, commercially available
10 from Pharmacia, Piscataway, NJ). The flow rate will be variable depending upon the column size.

The gel filtration step of the first method may be conducted in any suitable buffer (e.g., phosphate buffer saline) at a pH of preferably between about 7.0 and 7.5.
15 Suitable columns for use in this step include agarose-based, acrylamide-based, silica-based or polymer-based size-exclusion columns (e.g., columns of Sephadex G-75™ resin and Superdex-75™ resin, commercially available from Pharmacia).

20 In a particularly preferred embodiment of the second method, free sulfhydryl groups may be oxidized prior to the hydrophobic interaction step, discussed below. Any manner of oxidation may be employed. For example, the protein may be exposed to atmospheric
25 oxygen for a suitable period of time. Alternatively, various oxidation procedures may be employed. One such procedure is particularly suited for keratinocyte growth factors wherein one or more cysteine residues, as compared to the native KGF molecule, are deleted or
30 replaced. In this procedure an oxidizing agent (e.g., cystamine dihydrochloride or another appropriate oxidizing agent, for instance, cystine, oxidized glutathione or divalent copper) may be added to a final concentration, adjusting the pH to preferably between
35 about 7-9.5, with pH 9.0 ± 0.3 °C being more preferred when using cystamine dihydrochloride), and holding the

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temperature at preferably between about 10-30°C, for an appropriate period. The second procedure may be used for oxidizing native KGF and other keratinocyte growth factors with comparable patterns of cysteine residues.

5 In this procedure, oxidation may be accomplished by adding an appropriate amount of an ionic strength modifier (e.g., $(\text{NH}_4)_2\text{SO}_4$), adjusting the pH to preferably between about 7.5-9.5, and holding the temperature at preferably between about $23 \pm 5^\circ\text{C}$ for an
10 appropriate period.

The hydrophobic interaction step of the second method may be conducted by using any suitable buffer (e.g., sodium phosphate) at a pH of preferably between about 6.0-8.0, more preferably about 7.0, and by eluting
15 with a decreasing linear $(\text{NH}_4)_2\text{SO}_4$ gradient ranging from 2-0 M. Suitable columns for use in this step include alkyl or phenyl substituted resins (e.g., a column of Butyl-650M Toyopearl™ resin, commercially available from Tosohaas, Inc., Montgomeryville, PA and columns of
20 phenyl Sepharose™ resin and phenyl Superose™ resin, commercially available from Pharmacia).

The process of the present invention may be used to purify KGF. Thus, it should be understood that the terms "keratinocyte growth factor" and "KGF" as
25 employed in this description are intended to include, and to mean interchangeably unless otherwise indicated, native KGF and KGF analog proteins (or "muteins") characterized by a peptide sequence substantially the same as the peptide sequence of native KGF and by
30 retaining some or all of the biological activity of native KGF, particularly non-fibroblast epithelial cell proliferation (e.g., exhibiting at least about 500-fold greater stimulation of BALB/MK keratinocyte cells than that of NIH/3T3 fibroblast cells, and at least about 50-
35 fold greater stimulation of BALB/MK keratinocyte cells than for BS/589 epithelial cells or for CC1208

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epithelial cells, as determined by H-thymidine incorporation). By "characterized by a peptide sequence substantially the same as the peptide sequence of native KGF" is meant a peptide sequence which is encoded by a DNA sequence capable of hybridizing to nucleotides 201 to 684 of SEQ ID NO:1, preferably under stringent hybridization conditions.

The determination of a corresponding amino acid position between two amino acid sequences may be determined by aligning the two sequences to maximize matches of residues including shifting the amino and/or carboxyl terminus, introducing gaps as required and/or deleting residues present as inserts in the candidate. Database searches, sequence analysis and manipulations may be performed using one of the well-known and routinely used sequence homology/identity scanning algorithm programs (e.g., Pearson and Lipman (1988), *Proc. Natl. Acad. Sci. U.S.A.*, 85:2444-2448; Altschul et al. (1990), *J. Mol. Biol.*, 215:403-410; Lipman and Pearson (1985), *Science*, 222:1435 or Devereux et al. (1984), *Nuc. Acids Res.*, 12:387-395).

Stringent conditions, in the hybridization context, will be stringent combined conditions of salt, temperature, organic solvents and other parameters typically controlled in hybridization reactions. Exemplary stringent hybridization conditions are hybridization in 4 X SSC at 62-67° C., followed by washing in 0.1 X SSC at 62-67° C. for approximately an hour. Alternatively, exemplary stringent hybridization conditions are hybridization in 45-55% formamide, 4 X SSC at 40-45°C. [See, T. Maniatis et. al., *Molecular Cloning* (A Laboratory Manual); Cold Spring Harbor Laboratory (1982), pages 387 to 389].

Thus, the proteins include allelic variations, or deletion(s), substitution(s) or insertion(s) of amino acids, including fragments, chimeric or hybrid molecules

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of native KGF. One example of KGF includes proteins having residues corresponding to Cys¹ and Cys¹⁵ of SEQ ID NO:2 replaced or deleted, with the resultant molecule having improved stability as compared with the parent molecule (as taught in commonly owned U.S.S.N. 08/487,825, filed on July 7, 1995). Another example of KGF includes charge-change polypeptides wherein one or more of amino acid residues 41-154 of native KGF (preferably residues Arg⁴¹, Gln⁴³, Lys⁵⁵, Lys⁹⁵, Lys¹²⁸, Asn¹³⁷, Gln¹³⁸, Lys¹³⁹, Arg¹⁴⁴, Lys¹⁴⁷, Gln¹⁵², Lys¹⁵³ or Thr¹⁵⁴) are deleted or substituted with a neutral residue or negatively charged residue selected to effect a protein with a reduced positive charge (as taught in commonly owned U.S.S.N. 08/323,337, filed on October 13, 1994). A still further example of KGF includes proteins generated by substituting at least one amino acid having a higher loop-forming potential for at least one amino acid within a loop-forming region of Asn¹¹⁵-His¹¹⁶-Tyr¹¹⁷-Asn¹¹⁸-Thr¹¹⁹ of native KGF (as taught in commonly owned U.S.S.N. 08/323,473, filed on October 13, 1994). A still yet further example includes proteins having one or more amino acid substitutions, deletions or additions within a region of 123-133 (amino acids 154-164 of SEQ ID NO:2) of native KGF; these proteins may have agonistic or antagonistic activity.

Specifically disclosed proteins include the following KGF molecules (referred to by the residue found at that position in the mature protein (minus signal sequence) set forth in SEQ ID NO:2, followed by that amino acid position in parentheses and then either the substituted residue or "-" to designate a deletion): C(1,15)S, AN15-AN24, AN3/C(15)S, AN3/C(15)-, AN8/C(15)S, AN8/C(15)-, C(1,15)S/R(144)E, C(1,15)S/R(144)Q, AN23/R(144)Q, C(1,15,40)S, C(1,15,102)S, C(1,15,102,106)S, AN23/N(137)E, AN23/K(139)E, AN23/K(139)Q, AN23/R(144)A, AN23/R(144)E, AN23/R(144)L,

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ΔN23/K(147)E, ΔN23/K(147)Q, ΔN23/K(153)E, ΔN23/K(153)Q, ΔN23/Q(152)E/K(153)E; R(144)Q and H(116)G.

As those skilled in the art will also appreciate, a variety of host-vector systems may be utilized to express the KGF protein-coding sequence. These include but are not limited to eucaryotic cell systems such as mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast-containing yeast vectors; or to procaryotic cell systems such as bacteria transformed with bacteriophage DNA, plasmid DNA, or cosmid DNA. The expression elements of these vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

Once the protein product of KGF expression has been isolated, purified and assayed for KGF activity (using procedures known to those skilled in the art), it may be formulated in a variety of pharmaceutical compositions. Typically, such compositions include a suitable, usually chemically-defined, carrier or excipient for the therapeutic agent and, depending on the intended form of administration, other ingredients as well. The composition can include aqueous carriers or consist of solid phase formulations in which KGF is incorporated into non-aqueous carriers such as collagens, hyaluronic acid, and various polymers. The composition can be suitably formulated to be administered in a variety of ways, including by injection, orally, topically, intranasally and by pulmonary delivery.

Brief Description of the Drawings

Figure 1 shows the nucleotide (SEQ ID NO:1) and amino acid (SEQ ID NO:2) sequences of native KGF
5 (the nucleotides encoding the mature form of native KGF is depicted by bases 201 to 684 of SEQ ID NO:1 and the mature form of KGF is depicted by amino acid residues 32 to 194 of SEQ ID NO:2).

Figures 2A, 2B and 2C show the plasmid maps of
10 pCFM1156, pCFM1656 and pCFM3102, respectively.

Figure 3 shows the nucleotide (SEQ ID NO:3) and amino acid (SEQ ID NO:4) sequences of the construct RSH-KGF.

Figure 4 shows the nucleotide (SEQ ID NO:5) and amino acid (SEQ ID NO:6) sequences of the construct
15 contained in plasmid KGF.

Figure 5 shows the chemically synthesized OLIGOs (OLIGO#6 through OLIGO#11; SEQ ID NO:12-17, respectively) used to substitute the DNA sequence
20 between a *KpnI* site and an *EcoRI* site for a *KpnI* site (from amino acid positions 46 to 85 of SEQ ID NO:6) in the construct contained plasmid KGF to produce the construct in plasmid KGF(dsd).

Figure 6 shows the chemically synthesized
25 OLIGOs (OLIGO#12 through OLIGO#24; SEQ ID NO:18-30, respectively) used to construct KGF(codon optimized).

Figure 7 shows the nucleotide (SEQ ID NO:31) and amino acid sequences (SEQ ID NO:32) of C(1,15)S, a KGF analog having substitutions of serine for cysteine
30 at amino acid positions 1 and 15 of native KGF.

Figure 8 shows the nucleotide (SEQ ID NO:33) and amino acid sequences (SEQ ID NO:34) of C(1,15)S/R(144)E, a KGF analog having substitutions of serine for cysteine at amino acid positions 1 and 15 and
35 a substitution of glutamic acid for arginine at amino acid position 144 of native KGF.

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Figure 9 shows the nucleotide (SEQ ID NO:35) and amino acid (SEQ ID NO:36) sequences of C(1,15)S/R(144)Q, a KGF analog having substitutions of serine for cysteine at amino acid positions 1 and 15 and a substitution of glutamine for arginine at amino acid position 144 of native KGF.

Figure 10 shows the nucleotide (SEQ ID NO:37) and amino acid (SEQ ID NO:38) sequences of ΔN15, a KGF analog having a deletion of the first 15 amino acids of the N-terminus of native KGF.

Figure 11 shows the nucleotide (SEQ ID NO:39) and amino acid (SEQ ID NO:40) sequences of ΔN23, a KGF analog having a deletion of the first 23 amino acids of the N-terminus of native KGF.

Figure 12 shows the nucleotide (SEQ ID NO:41) and amino acid (SEQ ID NO:42) sequences of ΔN23/R(144)Q, a KGF analog having a deletion of the first 23 amino acids of the N-terminus and a substitution of glutamine for arginine at amino acid position 144 of native KGF.

Description of Specific Embodiments

Standard methods for many of the procedures described in the following examples, or suitable alternative procedures, are provided in widely recognized manuals of molecular biology such as, for example, *Molecular Cloning*, Second Edition, Sambrook et al., Cold Spring Harbor Laboratory Press (1987) and *Current Protocols in Molecular Biology*, Ausabel et al., Greene Publishing Associates/Wiley-Interscience, New York (1990).

Example 1: Preparation of DNA Coding for KGF and KGF Analogs

The cloning of the full-length human KGF gene (encoding a polypeptide with the sequence of native KGF)

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was carried out both by polymerase chain reaction (PCR) of RNA from an animal cell and by PCR of chemically synthesized (*E. coli* optimized codon) oligonucleotides ("OLIGOs"). Both procedures are described below:

5 PCR amplification using RNA isolated from cells known to produce the polypeptide was performed. Initially, cells from a human fibroblast cell line AG1523A (obtained from Human Genetic Mutant Cell Culture Repository Institute For Medical Research, Camden, New
10 Jersey) were disrupted with guanidium thiocyanate, followed by extraction (according to the method of Chomyszinski et al. (1987), *Anal. Biochem.*, 172:156). Using a standard reverse transcriptase protocol for total RNA, the KGF cDNA was generated. PCR (PCR#1)
15 amplification of the KGF gene was carried out using the KGF cDNA as template and primers OLIGO#1 and OLIGO#2 that encode DNA sequences immediately 5' and 3' of the KGF gene [model 9600 Thermocycler (Perkin-Elmer Cetus, Norwalk, CT); 28 cycles; each cycle consisting of one
20 minute at 94°C for denaturation, two minutes at 60°C for annealing, and three minutes at 72°C for elongation]. A small aliquot of the PCR#1 product was then used as template for a second KGF PCR (PCR#2) amplification identical to the cycle conditions described above except
25 for a 50°C annealing temperature. For expression cloning of the KGF gene, nested PCR primers were used to create convenient restriction sites at both ends of the KGF gene. OLIGO#3 and OLIGO#4 were used to modify the KGF DNA product from PCR#2 to include *MluI* and *BamHI*
30 restriction sites at the 5' and 3' ends of the gene, respectively [PCR#3; 30 cycles; each cycle consisting of one minute at 94°C for denaturation, two minutes at 60°C for annealing, and three minutes at 72°C for elongation]. This DNA was subsequently cut with *MluI*
35 and *BamHI*, phenol extracted and ethanol precipitated. It was then resuspended and ligated (using T4 ligase)

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into a pCFM1156 plasmid (Figure 2A) that contained a "RSH" signal sequence to make construct RSH-KGF (Figure 3). The ligation products were transformed (according to the method of Hanahan (1983), *J. Mol. Biol.*, 166:557) into *E. coli* strain FM5 (ATCC: 53911) and plated onto LB+kanamycin at 28°C. Several transformants were selected and grown in small liquid cultures containing 20 µg/mL kanamycin. The RSH-KGF plasmid was isolated from the cells of each culture and DNA sequenced. Because of an internal *NdeI* site in the KGF gene, it was not possible to directly clone the native gene sequence into the desired expression vector with the bracketed restriction sites of *NdeI* and *BamHI*. This was accomplished as a three-way ligation. Plasmid RSH-KGF was cut with the unique restriction sites of *BsmI* and *SstI*, and a ~3 kbp DNA fragment (containing the 3' end of the KGF gene) was isolated following electrophoresis through a 1% agarose gel. A PCR (PCR#4) was carried out as described for PCR#3 except for the substitution of OLIGO#5 for OLIGO#3. The PCR DNA product was then cut with *NdeI* and *BsmI* and a 311 bp DNA fragment was isolated following electrophoresis through a 4% agarose gel. The third fragment used in the ligation was a 1.8 kbp DNA fragment of pCFM1156 cut with *NdeI* and *SstI* isolated following electrophoresis through a 1% agarose gel. Following ligation (T4 ligase), transformation, kanamycin selection and DNA sequencing as described above, a clone was picked containing the construct in Figure 4, and the plasmid designated KGF. Because of an internal ribosomal binding site that produced truncated products, the KGF DNA sequence between the unique *KpnI* and *EcoRI* sites was replaced with chemically synthesized OLIGOs (OLIGO#6 through OLIGO#11) to minimize the use of the internal start site (Figure 5).

35

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OLIGO#1 (SEQ ID NO:7): 5'-CAATGACCTAGGAGTAACAATCAAC-3'
OLIGO#2 (SEQ ID NO:8): 5'-AAAACAAACATAAATGCACAAGTCCA-3'
OLIGO#3 (SEQ ID NO:9): 5'-ACAACGCGTGCAATGACATGACTCCA-3'
OLIGO#4 (SEQ ID NO:10):
5 - 5'-ACAGGATCCTATTAAGTTATTGCCATAGGAA-3'
OLIGO#5 (SEQ ID NO:11):
5'-ACACATATGTGCAATGACATGACTCCA-3'
OLIGO#6 (SEQ ID NO:12):
5'-CTGCGTATCGACAAACGCGGCAAAGTCAAGGGCACCC-3'
10 OLIGO#7 (SEQ ID NO:13):
5'-AAGAGATGAAAAACAACACTACAATATTATGGAATCCGTACTGTT-3'
OLIGO#8 (SEQ ID NO:14):
5'-GCTGTTGGTATCGTTGCAATCAAAGGTGTTGAATCTG-3'
OLIGO#9 (SEQ ID NO:15):
15 5'-TCTTGGGTGCCCTTGACTTTGCCGCGTTTGTGATACGCAGGTAC-3'
OLIGO#10 (SEQ ID NO:16):
5'-ACAGCAACAGTACGGATTTCCTAATATTGTAGTTGTTTTTCATC-3'
OLIGO#11 (SEQ ID NO:17):
5'-AATTCAGATTCAACACCTTTGATTGCAACGATACCA-3'

20

The OLIGOs were phosphorylated with T4 polynucleotide kinase and then heat denatured. The single-stranded (ss) OLIGOs were then allowed to form a ds DNA fragment by allowing the temperature to slowly
25 decrease to room temperature. T4 ligase was then used to covalently link both the internal OLIGO sticky-ends and the whole ds OLIGO fragment to the KGF plasmid cut with *KpnI* and *EcoRI*. The new plasmid was designated KGF(dsd).

30

A completely *E. coli* codon-optimized KGF gene was constructed by PCR amplification of chemically synthesized OLIGOs #12 through 24.

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OLIGO#12 (SEQ ID NO:18): 5'-AGTTTTGATCTAGAAGGAGG-3'
 OLIGO#13 (SEQ ID NO:19): 5'-TCAAACTGGATCCTATTAA-3'
 OLIGO#14 (SEQ ID NO:20):
 5'-AGTTTTGATCTAGAAGGAGGAATAACATATGTGCAACGACATGAC-
 5 TCCGGAACAGATGGCTACCAACGTTAAGTCTCCAGCCCGGAACGT-3'
 OLIGO#15 (SEQ ID NO:21):
 5'-CACACCCGTAGCTACGACTACATGGAAGGTGGTGACATCCGTGTTT-
 GTCGTCTGTTCTGCCGTACCCAGTGGTACCTGCGTATCGACAAA-3'
 OLIGO#16 (SEQ ID NO:22):
 10 5'-CGTGGTAAAGTTAAAGGTACCCAGGAAATGAAAAACAATA-
 CAACATCATGGAAATCCGTACTGTTGCTGTTGGTATCGTTGCAATCAAA-3'
 OLIGO#17 (SEQ ID NO:23):
 5'-GGTGTGAATCTGAATCTACCTGGCAATGAACAAAGAAGGTAAAC-
 TGTACGCAAAAAAGAATGCAACGAAGACTGCAACTTCAAGAA-3'
 15 OLIGO#18 (SEQ ID NO:24):
 5'-CTGATCCTGGAACCACTACAACACCTACGCATCTGCTAAATGGA-
 CCCACAACGGTGGTGAATGTTGCTGCTGAACCAGAAAGGT-3'
 OLIGO#19 (SEQ ID NO:25):
 5'-ATCCCGGTTCTGTTGTTAAAAAACCAAAAAAGAACAGAAAACCGCT-
 20 CACTTCCTGCCGATGGCAATCACTTAATAGGATCCAGTTTGA-3'
 OLIGO#20 (SEQ ID NO:26): 5'-TACGGGTGTGACGTTCCGGG-3'
 OLIGO#21 (SEQ ID NO:27): 5'-CTTTACCACGTTTGTGCGATA-3'
 OLIGO#22 (SEQ ID NO:28): 5'-ATTCAACACCTTTGATGCA-3'
 OLIGO#23 (SEQ ID NO:29): 5'-CCAGGATCAGTTCTTTGAAG-3'
 25 OLIGO#24 (SEQ ID NO:30): 5'-GAACCGGGATACCTTTCTGG-3'

OLIGOs #12 through 24 were designed so that
 the entire DNA sequence encoding native KGF was
 represented by OLIGOs from either the "Watson" or the
 30 "Crick" strand and upon PCR amplification would produce
 the desired double-stranded DNA sequence (Figure 6)
 [PCR#5, Model 9600 thermocycler (Perkin-Elmer Cetus); 21
 cycles, each cycle consisting of 31 seconds at 94°C for
 denaturation, 31 seconds at 50°C for annealing, and 31
 35 seconds at 73°C for elongation; following the 21 cycles
 the PCR was finished with a final elongation step of 7

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minutes]. After PCR amplification, the DNA fragment was cut with *Xba*I and *Bam*HI and the 521 bp fragment ligated into the expression plasmid pCFM1156 cut with the same enzymes. PCR#5 utilized the outside primers

5 (100 pmoles/100 µl rxn) OLIGO#12 and OLIGO#13 and 1 µl/100 µl rxn of a KGF template derived by ligation (by T4 ligase) of OLIGOs #14 through #19 (OLIGOs#15 through OLIGOs#18 were phosphorylated with T4 polynucleotide kinase) using OLIGOs#20 through OLIGOs#24

10 as band-aid oligos (Jayaraman et al. (1992), *Biotechniques*, 12:392) for the ligation. The final construct was designated KGF(codon optimized).

All of the KGF analogs described herein are composed in part from DNA sequences found in KGF(dsd) or

15 KGF(codon optimized), or a combination of the two. The sequences are further modified by the insertion into convenient restrictions sites of DNA sequences that encode the particular KGF analog amino acids made utilizing one or more of the above-described techniques

20 for DNA fragment synthesis. Any of the analogs can be generated in their entirety by either of the above described techniques. However, as a part of the general OLIGO design optimized *E. coli* codons were used where appropriate, although the presence of *E. coli* optimized

25 codons in part or in toto of any of the genes where examined did not significantly increase the yield of protein that could be obtained from cultured bacterial cells. Figures 7 to 12 set forth by convenient example particular KGF analog nucleotide and amino acid sequence

30 constructions: C(1,15)S (Figure 7); C(1,15)S/R(144)E (Figure 8); C(1,15)S/R(144)Q (Figure 9); AN15 (Figure 10); AN23 (Figure 11) and AN23/R(144)Q (Figure 12). All the KGF analog constructions described herein were DNA sequence confirmed.

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Example 2: Purification from E. coli

Three different expression plasmids were
5 utilized in the cloning of the KGF analog genes. They
were pCFM1156 (ATCC 69702), pCFM1656 (ATCC 69576), and
pCFM3102 (Figures 2A, 2B and 2C, respectively). The
plasmid p3102 can be derived from the plasmid pCFM1656
by making a series of site directed base changes with
10 PCR overlapping oligo mutagenesis. Starting with the
BglII site (pCFM1656 plasmid bp #180) immediately 5' to
the plasmid replication promoter, P_{copB}, and proceeding
toward the plasmid replication genes, the base pair
changes are as follows:

15

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	<u>pCFM1656 bp #</u>	<u>bp in pCFM1656</u>	<u>bp changed to in pCFM3102</u>
	# 204	T/A	C/G
	# 428	A/T	G/C
	# 509	G/C	A/T
5	# 617	- -	insert two G/C bp
	# 677	G/C	T/A
	# 978	T/A	C/G
	# 992	G/C	A/T
	# 1002	A/T	C/G
10	# 1005	C/G	T/A
	# 1026	A/T	T/A
	# 1045	C/G	T/A
	# 1176	G/C	T/A
	# 1464	G/C	T/A
15	# 2026	G/C	bp deletion
	# 2186	C/G	T/A
	# 2479	A/T	T/A
	# 2498-2501	<u>AGTG</u>	<u>GTCA</u>
20		TCAC	CAGT
	# 2641-2647	<u>TCCGAGC</u>	bp deletion
		AGGCTCG	
25	# 3441	G/C	A/T
	# 3452	G/C	A/T
	# 3649	A/T	T/A
	# 4556	--	insert bps
30		(SEQ ID NO:43) 5'- <u>GAGCTCACTAGTGTCTCGACCTGCAG</u> -3'	
		(SEQ ID NO:44) 5'-CTCGAGTGATCACAGCTGGACGTC-3'	

As seen above, pCFM1156, pCFM1656 and pCFM3102 are very similar to each other and contain many of the same restriction sites. The plasmids were chosen by convenience, and the vector DNA components can be easily exchanged for purposes of new constructs. The host used for all cloning was *E. coli* strain FM5 (ATCC: 53911) and the transformations were carried out (according to the method of Hanahan (1983), *supra*) or by electroelution with a Gene Pulser[™] transfection apparatus (BioRad Laboratories, Inc., Hercules, CA), according to the manufacturer's protocol.

Initially, a small, freshly-cultured inoculum of the desired recombinant *E. coli* clone harboring the

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desired construct on one of the three pCFM vectors was started by transferring 0.1 mL of a frozen glycerol stock of the appropriate strain into a 2 L flask containing 500 mL of Luria broth. The culture was
5 shaken at 30°C for 16 hours. Thereafter the culture was transferred to a 15 L fermentor containing 8 L of sterile batch medium (Tsai, et al. (1987), *J. Industrial Microbiol.*, 2:181-187).

Feed batch fermentation starts with the
10 feeding of Feed # 1 medium (Tsai, et al. (1987.), *supra*). When the OD600 reached 35, expression of the desired KGF analog was induced by rapidly raising the culture temperature to 37°C to allow the amplification of plasmid. After two hours at 37°C, the culture
15 temperature was quickly raised to 42°C to denature the CI repressor and the addition of Feed 1 was discontinued in favor of Feed 2, the addition rate of which was initiated at 300 mL/hr. Feed 2 comprised 175 g/L trypticase-peptone, 87.5 g/L yeast extract, and 260 g/L
20 glucose. After one hour at 42°C, the culture temperature was decreased to 36°C, where this temperature was then maintained for another 6 hours.

The fermentation was then halted and the cells were harvested by centrifugation into plastic bags
25 placed within 1 L centrifuge bottles. The cells were pelleted by centrifugation at 400 rpm for 60 minutes, after which the supernatants were removed and the cell paste frozen at -90°C.

Following expression of the various KGF
30 analogs in *E. coli*, native KGF, C(1,15)S, C(1,15)S/R(144)E, C(1,15)S/R(144)Q, ΔN15, ΔN23, and ΔN23/R(144)Q protein were purified using the following procedure. Cell paste from a high cell density fermentation was suspended at 4°C in 0.2 M NaCl, 20 mM
35 NaPO₄, pH 7.5 as a 10-20% solution (weight per volume) using a suitable high shear mixer. The suspended cells

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were then lysed by passing the solution through a homogenizer (AFV Gaulin, Inc., Everett, MA) three times. The outflowing homogenate was cooled to 4-8°C by using a suitable heat exchanger. Debris was then removed by centrifuging the lysate in a J-6B™ centrifuge (Beckman Instruments, Inc., Brea, CA) equipped with a JS 4.2 rotor at 4,200 rpm for 30-60 min. at 4°C. Supernatants were then carefully decanted and loaded onto a previously prepared 450 mL (5 cm x 23 cm) column of S-Sephacrose Fast Flow™ resin (Pharmacia) column equilibrated with 0.2 M NaCl, 20 mM NaPO₄, pH 7.5 at 4°C. Next, the column was washed with five column volumes (2250 mL) of 0.4 M NaCl, 20 mM NaPO₄, pH 7.5 at 4°C. The desired protein was eluted by washing the column with 5 L of 0.5 M NaCl, 20 mM NaPO₄, pH 7.5. Again, 50 mL fractions were collected and the A₂₈₀ of the effluent was continuously monitored. Fractions identified by A₂₈₀ as containing eluted material were then analyzed by SDS-PAGE through 14% gels to confirm the presence of the desired polypeptide.

Those fractions containing proteins of interest were then pooled, followed by the addition of an equal volume of distilled water. The diluted sample was then loaded onto a previously prepared 450 mL (5 cm x 23 cm) column of S-Sephacrose Fast Flow equilibrated with 0.4 M NaCl, 20 mM NaPO₄, pH 6.8 at 4°C. The column was washed with 2250 mL of 0.4 M NaCl, 20 mM NaPO₄, pH 6.8 and the protein eluted using a 20 column volume linear gradient ranging from 0.4 M NaCl, 20 mM NaPO₄, pH 6.8 to 0.6 M NaCl, 20 mM NaPO₄, pH 6.8. Again, 50 mL fractions were collected under constant A₂₈₀ monitoring of the effluent. Those fractions containing the protein (determined by 14% SDS-PAGE) were then pooled, followed by concentration through a YM-10 membrane (10,000 molecular weight cutoff) in a 350cc stirring cell (Amicon, Inc. Mayberry, MA) to a volume of 30-40 mL.

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The concentrate was then loaded onto a previously generated 1,300 mL (4.4 cm x 85 cm) column of Superdex-75™ resin (Pharmacia) equilibrated in column buffer comprising 1X PBS (Dulbecco's Phosphate Buffered Saline, "D-PBS," calcium and magnesium-free) or 0.15 M NaCl, 20 mM NaPO₄, pH 7.0. After allowing the sample to run into the column, the protein was eluted from the gel filtration matrix using column buffer. Thereafter, 10 mL fractions were recovered and those containing the analog (determined by 14% SDS-PAGE) were pooled. Typically, the protein concentration was about 5-10 mg/mL in the resultant pool. All of the above procedures were performed at 4-8°C, unless otherwise specified.

15 An alternative purification procedure was used to purify native KGF, C(1,15)S and AN23. The procedure involves the following steps and, unless otherwise specified, all procedures, solutions and materials were conducted at 23 ± 5°C.

20 Upon completion of the production phase of a bacterial fermentation, the cell culture was cooled to 4-8°C and the cells were harvested by centrifugation or a similar process. On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, was suspended in a mild buffer solution, 20 mM NaPO₄, 0.2 M NaCl, pH 7.5, weighing about five times that of the cell paste to be suspended. The cells were dispersed to a homogeneous solution using a high shear mixer. The temperature of the cell paste dispersion was maintained at 4-8°C during homogenization.

30 The cells were then lysed by pressure, for example by passing the cell paste dispersion twice through an appropriately sized cell homogenizer. The homogenate was kept chilled at 5 ± 3°C. To clarify the

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cell lysate, a previously prepared depth filter housing (Cuno, Inc., Meriden, CT) equipped with a filter having an appropriate amount of filter surface area, equilibrated with a suitable volume of 0.2 M NaCl, 20 mM NaPO₄, pH 7.5 was employed. The equilibration and clarification were performed at $5 \pm 3^\circ\text{C}$. Prior to clarification, an appropriate amount of a suitable filter aid was used to pre-coat the filter and be thoroughly mixed with the cell lysate, after which the lysate was clarified by passing the solution through the filter apparatus. The filter was washed with 0.2 M NaCl, 20 mM NaPO₄, pH 7.5. The filtrate and any subsequent wash were collected in a chilled container of suitable capacity, all the while being maintained at less than 10°C .

Following clarification the lysate was then passed through a previously prepared column of SP-Sepharose Fast Flow containing at least 1 mL of resin per 2 g of cell paste. The column of SP-Sepharose Fast Flow was equilibrated with cold ($5 \pm 3^\circ\text{C}$), 0.2 M NaCl, 20 mM NaPO₄, pH 7.5. The temperature of the column was maintained at less than 10°C . The clarified lysate ($5 \pm 3^\circ\text{C}$) was then loaded onto the ion exchange column, with the absorbance at 280 nm (A_{280}) of eluate being continuously monitored. After sample loading, the column was washed with cold 0.2 M NaCl, 20 mM NaPO₄, pH 7.5, followed by washing with 0.3 M NaCl, 20 mM NaPO₄, pH 7.5 at $23 \pm 5^\circ\text{C}$.

To elute the desired protein, a linear gradient ranging from 0.2-1 M NaCl, 20 mM NaPO₄, pH 7.5 was used. Bulk product was collected in several fractions on the basis of the A_{280} of the eluate. Following elution, these fractions were pooled and the volume noted.

To oxidize free sulfhydryl groups, an oxidation step was performed. For proteins with altered

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cysteine patterns, as compared to native KGF, an oxidizing agent (e.g., cystamine dihydrochloride or another appropriate oxidizing agent, for instance, cystine, oxidized glutathione or divalent copper) was added to a final concentration of 1-20 mM and the pH was adjusted to 7-9.5, with a pH of 9.0 ± 0.3 when cystamine dihydrochloride was used. The oxidation was conducted at 10 - 30°C for an appropriate period. For the native KGF protein, oxidation was accomplished by adding an appropriate amount of $(\text{NH}_4)_2\text{SO}_4$ such as 1-2 M $(\text{NH}_4)_2\text{SO}_4$, adjusting the pH to 7.5-9.5, and holding the temperature at $23 \pm 5^\circ\text{C}$ for an appropriate period.

After oxidation, the pH of the solution was adjusted to between 6.5 and 9.5. If necessary, solid $(\text{NH}_4)_2\text{SO}_4$ was added to the solution to a final concentration of 2 M. To remove particulates, the solution was passed through appropriate clarification filters.

The filtered, oxidized product was then subjected to hydrophobic interaction chromatography (HIC). The HIC matrix was Butyl-650M Toyopearl™ resin (Tosohaas, Inc., Montgomeryville, PA). The protein-containing solution was loaded onto the column, which had been previously equilibrated with 2 M $(\text{NH}_4)_2\text{SO}_4$, 0.15 M NaCl, 20 mM NaPO_4 , pH 7.0. After sample loading, the column was washed with 2 M $(\text{NH}_4)_2\text{SO}_4$, 0.15 M NaCl, 20 mM NaPO_4 , pH 7.0. The desired protein was then eluted using a decreasing linear $(\text{NH}_4)_2\text{SO}_4$ gradient ranging from 2-0 M developed in 0.15 M NaCl, 20 mM NaPO_4 , pH 7.0. When the desired protein began to elute, as indicated by an increase in the A_{280} of the eluate, fractions were collected. Aliquots of each fraction were then analyzed by SDS-PAGE. Those fractions containing the desired protein were then pooled, thoroughly mixed, and the volume of the pool determined, as was the concentration of the protein therein.

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The pooled HIC protein-containing eluate was then concentrated and the elution buffer exchanged. Typically, proteins were concentrated to 5.0-10.0 mg/mL. Ultrafiltration was conducted using an ultrafiltration system equipped with a Pellicon[™] cassette system (Millipore, Inc., Bedford, MA) with an appropriately sized cut-off membrane

After concentration, the sample was diafiltered against an appropriate buffer. The retentate from the concentration step was diafiltered against 0.15 M NaCl, 20 mM NaPO₄, pH 7.0 until the conductivity of the retentate was within 5% of the conductivity of the 0.15 M NaCl, 20 mM NaPO₄, pH 7.0 solution.

In addition, to remove precipitates and bacterial endotoxin that might be present, the concentrated diafiltered protein-containing sample was passed through a 0.1 µm Posidyne[™] filter (Pall, Inc., Cortland, NY). After determining the protein concentration of the solution and on the basis of the desired concentration of the final bulk product, the solution was diluted with 0.15 M NaCl, 20 mM sodium phosphate, pH 7.0, to the desired final concentration. A final aseptic filtration through a 0.22 µm filter, was then performed as the final bulk product was transferred to a pyrogen-free container for storage (at about 5°C) for further formulation.

Example 3: Purification from Mammalian Cell Culture

This example describes the expression, isolation, and characterization of two biologically active recombinant KGF (rKGF) forms produced in a mammalian expression system.

The human KGF gene was isolated by PCR amplification of cDNA made from normal dermal human

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fibroblast cells (Clonetec, Inc., Palo Alto, CA). Following the making of cDNA by reverse transcriptase, PCR was used to amplify the KGF gene. OLIGO#25 and OLIGO#26 were used to amplify the gene out of the cDNA and OLIGO#27 and OLIGO#28 were used to place *Hind*III and *Bgl*III restriction sites at the fragment ends by a second PCR amplification, as set forth in Figure 1.

OLIGO#25 (SEQ ID NO:45): 5'-CAATCTACAATTCACAGA-3'
10 OLIGO#26 (SEQ ID NO:46): 5'-TTAAGTTATTGCCATAGG-3'
OLIGO#27 (SEQ ID NO:47): 5'-AACAAAGCTTCTACAATTCACAGATAGGA-3'
OLIGO#28 (SEQ ID NO:48): 5'-AACAAAGATCTTAAGTTATTGCCATAGG-3'

Following cloning and DNA sequence
15 confirmation, the KGF gene DNA was then used.
Amplification was effected using two primers:

OLIGO#29 (SEQ. ID. NO:49):
5'-CGGTCTAGACCACCATGCACAAATGGATACTGACATGG-3'
20 OLIGO#30 (SEQ. ID. NO:50):
5'-GCCGTCGACCTATTAAGTTATTGCCATAGGAAG-3'

The sense primer, OLIGO#29, included an *Xba*I site and a consensus Kozak translation sequence (5'-
25 CCACC-3') upstream of the start codon, ATG. The
antisense primer, OLIGO#30, included a *Sal*I cloning
site and an additional stop codon. After 18 cycles of
PCR amplification (30 sec. denaturation at 94°C, 40 sec.
annealing at 55°C, and 40 sec. elongation at 72°C), the
30 product was digested with *Xba*I and *Sal*I and ligated with
a similarly digested DNA of pDSR α 2 (according to the
methods of Bourdrel et al. (1993), Protein Exp. &
Purif., 4:130-140 and Lu et al. (1992), Arch. Biochem.
Biophys., 298:150-158). This resulted in plasmid
35 KGF/pDSR α 2 which placed the human KGF gene between the
SV40 early promoter and the α -FSH polyadenylation

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sequences. Two clones were picked and DNA sequence analysis confirmed construction of the desired vector.

Two micrograms of KGF/pDSR α 2 DNA were then linearized with PvuI. Chinese hamster ovary (CHO) cells, seeded the day before at 0.8×10^6 cells/60 mm culture dish, were then transfected with the treated DNA using a standard calcium phosphate precipitation method (Bourdrel et al., supra). Two weeks later, individual colonies were picked and transferred into 24-well plates. The conditioned media was considered serum-free when the cells reached confluency and aliquots thereof were analyzed by Western blotting using a polyclonal rabbit antiserum reactive against *E. coli*-expressed human KGF.

Westerns were performed by running samples through 12.5% (w/v) SDS polyacrylamide gels, followed by electroblotting for 1 hr. at 400 mA onto nitrocellulose membranes using a semidry transfer apparatus (Hoefer Scientific Instruments, San Francisco, CA). 20 mM Tris, 150 mM glycine, 20% methanol served as the transfer buffer. The nitrocellulose sheets were blocked by incubation with 10% normal goat serum in PBS. Rabbit anti-serum raised against *E. coli*-derived KGF was used as primary antibody. For use, it was diluted 1/10,000 in 1% normal goat serum in PBS and incubated with the blocked nitrocellulose sheets for 12 hr. at room temperature, after which excess antibody was removed by three 30 min. washes in PBS. The nitrocellulose membranes were then incubated in 100 mL of 1% normal goat serum in PBS containing VectastainTM biotinylated goat anti-rabbit IgG (secondary antibody, Vector Labs, Burlingame, CA), for 30 minutes at room temperature. After three 10 minute washes in PBS, a 30 minute room temperature incubation was performed in a 100 mL solution of 1% normal goat serum containing streptavidin and biotinylated peroxidase, prepared according to

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manufacturer's directions (Vector Labs). Following three washes in PBS, KGF cross-reactive material was visualized by incubation in a mixture of 60 μ L of 30% (w/v) H_2O_2 in 100 mL of PBS and 50 mg of 4-chloronapthol in 20 mL of methanol. The reaction was stopped by rinsing in water after 10 minutes.

Analysis of the blots revealed that the KGF-specific antibody associated with three distinct protein bands, two being closely related with molecular weights of about 25-29 kDa and one with an estimated molecular weight of about 17 kDa, as compared to the expected molecular weight of approximately 18.8 of the 163 amino acid mature protein. Additionally, several high expressing clones secreting more than 2.0 mg of rKGF per liter, as judged by Western analysis, were selected and expanded into roller bottles (according to the method of Lu et al., supra) to generate large volumes of serum-free conditioned medium for purification of KGF by cationic exchange chromatography and gel filtration, as set forth below.

KGF from 3 L of serum-free conditioned medium was purified applying the medium directly to a cation exchange column (5 x 24 cm) packed with 450 mL of sulfoethyl column of SP-Sepharose Fast Flow (Pharmacia) pre-equilibrated with 20 mM sodium phosphate, pH 7.5. After washing with five column volumes of 20 mM sodium phosphate, 0.2 M NaCl, pH 7.5, rKGF was eluted using a 20 column volume linear gradient of 0.2 to 1.0 M NaCl in 20 mM sodium phosphate, pH 7.5. 50 mL fractions were collected with continuous A_{280} monitoring. KGF protein was detected by analyzing aliquots of each fraction by SDS-PAGE. SDS-PAGE was performed on an electrophoresis system (Novex, San Diego, CA) using precast 14% Tris-glycine precast gels (according to the method of Laemmli (1970), Nature, 227:680-685). Samples were mixed with non-reducing SDS sample buffer without

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heating before loading. The proteins were detected by either Coomassie blue or silver staining. Two late-eluting peaks were seen to contain protein bands corresponding to the 25-29 kDa and 17 kDa bands detected by Western blot. The fractions containing each of these peaks were separately concentrated to a volume of less than 1.0 mL and subjected to gel filtration.

The gel filtrations employed columns of Superdex-75™ resin (HR 10/30, Pharmacia) pre-equilibrated with PBS, pH 7.2, and calibrated with the following known molecular weight standards (BioRad, San Francisco, CA): thyroglobulin (670 kDa), gamma globulin (158 kDa), ovalbumin (44 kDa), myoglobin (17 kDa) and vitamin B-12 (1.4 kDa). These purification steps resulted in an approximate 2000-fold purification of rKGF, specifically including a 17 kDa and a 30 kDa material, as estimated by silver staining.

In the instance of the higher molecular weight material, rKGF eluted as a major symmetrical peak, which was called KGF-a. Upon SDS-PAGE analysis of a lesser amount of this material, 3 µg/lane versus 6 µg/lane, two bands with a 1-2 kDa molecular weight difference were resolved. In the instance of the lower molecular weight material, termed KGF-b, gel filtration resulted in a protein preparation having the expected mobility. For both KGF-a and KGF-b, the overall yield after purification was approximately 30-40%.

Amino acid sequences from KGF-a and KGF-b were also analyzed. These analyses were performed on an automatic sequencer (Model 477A or 470A, Applied Biosystems, Inc., Foster City, CA) equipped with a Model 120A on-line PTH-amino acid analyzer and a Model 900A data collection system (according to the method of Lu et al. (1991), *J. Biol. Chem.*, 266:8102-8107). Edman sequence analysis of KGF-a revealed a major N-terminal sequence of X₁-N-D-M-T-P-E-Q-M-A-T-N-V-X₂-X₃-S- (SEQ ID

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NO:51). A minor sequence starting from the third N-terminal amino acid, aspartic acid, was also present in 1.6% of the total sequenceable protein. X₁, X₂, and X₃ were the unassigned due to the absence of
5 phenylthiohydantoinyl (PTH) amino acid signals during sequence analysis.

Interestingly, N-terminal sequence analysis of KGF-b revealed an N-terminal amino acid sequence of S-Y-D-Y-M-E-G-G-D-I-R-V- (SEQ ID NO:52), indicating that
10 it is an N-terminally truncated form of KGF that has been proteolytically cleaved at the Arg²³-Ser²⁴ peptide bond.

To further characterize purified KGF-a and KGF-b, the protein was subjected to glycosidases
15 (neuraminidase, O-glycanase, and/or N-glycanase), using known techniques (Sasaki et al. (1987), *J. Biol. Chem.*, 262:12059-12076; Takeuchi et al. (1988), *J. Biol. Chem.*, 263:3657-3663; Zsebo et al. (1990), *Cell*, 63:195-201). These data indicate that KGF-a contains N- and O-linked
20 carbohydrates, although the lower molecular weight form of KGF-a probably contains only N-linked sugar. Glycosidase treatment did not cause molecular weight reduction for KGF-b, indicating that the molecule is unglycosylated.

25

Example 4: Biological Activity

Each KGF analog was diluted and assayed for biological activity by measuring the [³H]-thymidine
30 uptake of Balb/MK cells (according to the method of Rubin et al. (1989), *supra*). The samples were first diluted in a bioassay medium consisting of 50% customer-made Eagle's MEM, 50% customer-made F12, 5 µg/mL transferrin, 5 ng/mL sodium selenite, 0.0005% HSA and
35 0.005% Tween 20. KGF samples were then added into Falcon primeria 96-well plates seeded with Balb/MK

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cells. Incorporation of [^3H]-Thymidine during DNA synthesis was measured and converted to input native KGF concentration by comparison to a native KGF standard curve. Each of the tested analogs exhibited mitogenic activity.

Interaction with the KGF receptor was examined using isolated KGF receptor membrane preparations prepared from Balb/MK mouse epidermal keratinocytes (by the procedure described by Massague (19932), *J. Biol. Chem.*, 258:13614-13620). Specifically, various forms of KGF were diluted with 50 mM Tris-HCl, pH 7.5, containing 0.2% bovine serum albumin so as to range in concentration from 0.8 ng to 100 ng per 50 μL . They were individually incubated with the membrane preparation (75 ng/mL) and ^{125}I -labeled *E. coli*-derived KGF (1.5 ng). Receptor binding and competition experiments were performed at 4°C for 16 hr., after which time samples were taken, centrifuged, and washed twice with the above diluent buffer to remove unbound and non-specifically bound, labeled KGF. Samples were then counted for the remaining radioactivity. Competition curves for receptor binding between KGF samples and labeled KGF were constructed by plotting percent uncompetition versus concentrations of each KGF sample. Radioreceptor assay uncompetition experiments indicated that *E. coli*-derived KGF, KGF-a, and KGF-b have similar receptor binding activity.

While the present invention has been described above both generally and in terms of preferred embodiments, it is understood that other variations and modifications will occur to those skilled in the art in light of the description above.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Amgen Inc.

(ii) TITLE OF INVENTION: Method for Purifying Keratinocyte Growth Factors

(iii) NUMBER OF SEQUENCES: 52

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
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(C) CITY: Thousand Oaks
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(E) COUNTRY: U.S.A.
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/487,830
(B) FILING DATE:
(C) CLASSIFICATION: not yet known

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATCTACAA TTCACAGATA GGAAGAGGTC AATGACCTAG GAGTAACAAT CAACTCAAGA	60
TTCATTTTCA TTATGTTATT CATGAACACC CGGAGCACTA CACTATAATG CACAAATGGA	120
TACTGACATG GATCCTGCCA ACTTTGCTCT ACAGATCATG CTTTCACATT ATCTGTCTAG	180
TGGGTACTAT ATCTTTAGCT TGCAATGACA TGACTCCAGA GCAAATGGCT ACAAATGTGA	240
ACTGTTCCAG CCCTGAGCGA CACACAAGAA GTTATGATTA CATGGAAGGA GGGGATATAA	300

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GAGTGAGAAG ACTCTTCTGT CGAACACAGT GGTACCTGAG GATCGATAAA AGAGGCAAAG 360
TAAAAGGGAC CCAAGAGATG AAGAATAATT ACAATATCAT GGAAATCAGG ACAGTGGCAG 420
TTGGAATTGT GGCAATCAAA GGGGTGGAAA GTGAATTCTA TCTTGCAATG AACAAGGAAG 480
GAAACTCTA TGCAAAGAAA GAATGCAATG AAGATTGTAA CTTCAAAGAA CTAATTCTGG 540
AAAACCATTA CAACACATAT GCATCAGCTA AATGGACACA CAACGGAGGG GAAATGTTTG 600
TTGCCCTTAAA TCAAAAGGGG ATTCCTGTAA GAGGAAAAAA AACGAAGAAA GAACAAAAAA 660
CAGCCCACTT TCTTCCTATG GCAATAACTT AATTGCATAT GGTATATAAA GAACCCAGTT 720
CCAGCAGGGA GATTTCTTTA AGTGGACTGT TTTCTTTCTT CTCAAAATTT TCTTTCCTTT 780
TATTTTTTAG TAATCAAGAA AGGCTGGAAA AACTACTGAA AACTGATCA AGCTGGACTT 840
GTGCATTAT GTTTGTTTAA AG 862

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg
1 5 10 15
Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
20 25 30
Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser
35 40 45
Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
50 55 60
Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp
65 70 75 80
Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn
85 90 95
Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
100 105 110
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr
115 120 125

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Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
 130 135 140

Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly
 145 150 155 160

Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly
 165 170 175

Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala
 180 185 190

Ile Thr

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 595 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATCGATTGGA TTCTAGAAGG AGGAATAACA TATGAAAAAG CGCGCACGTG CTATCGCCAT	60
TGCTGTGGCT CTGGCAGGTT TCGCAACTAG TGCAACGCG TGCAATGACA TGAATCCAGA	120
GCAATGGCT ACAATGTGA ACTGTTCCAG CCCTGAGCGA CACACAAGAA GTTATGATTA	180
CATGGAAGGA GGGGATATAA GAGTGAGAAG ACTCTTCTGT CGAACACAGT GGTACCTGAG	240
GATCGATAAA AGAGGCAAAG TAAAGGGAC CCAAGAGATG AAGAATAATT ACAATATCAT	300
GGAAATCAGG ACAGTGGCAG TTGGAATTGT GGCAATCAAA GGGGTGGAAA GTGAATTCTA	360
TCTTGCAATG AACAGGAAG GAAACTCTA TGCAAAGAAA GAATGCAATG AAGATTGTAA	420
CTTCAAAGAA CTAATTCTGG AAAACCATTAA CAACACATAT GCATCAGCTA AATGGACACA	480
CAACGGAGGG GAAATGTTTG TTGCCTTAAA TCAAAGGGG ATTCCTGTAA GAGGAAAAAA	540
AACGAAGAAA GAACAAAAAA CAGCCCACTT TCTTCTATG GCAATAACTT AATAG	595

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Lys Arg Ala Arg Ala Ile Ala Ile Ala Val Ala Leu Ala Gly
 1 5 10 15
 Phe Ala Thr Ser Ala His Ala Cys Asn Asp Met Thr Pro Glu Gln Met
 20 25 30
 Ala Thr Asn Val Asn Cys Ser Ser Pro Glu Arg His Thr Arg Ser Tyr
 35 40 45
 Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg Arg Leu Phe Cys Arg
 50 55 60
 Thr Gln Trp Tyr Leu Arg Ile Asp Lys Arg Gly Lys Val Lys Gly Thr
 65 70 75 80
 Gln Glu Met Lys Asn Asn Tyr Asn Ile Met Glu Ile Arg Thr Val Ala
 85 90 95
 Val Gly Ile Val Ala Ile Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala
 100 105 110
 Met Asn Lys Glu Gly Lys Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp
 115 120 125
 Cys Asn Phe Lys Glu Leu Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala
 130 135 140
 Ser Ala Lys Trp Thr His Asn Gly Gly Glu Met Phe Val Ala Leu Asn
 145 150 155 160
 Gln Lys Gly Ile Pro Val Arg Gly Lys Lys Thr Lys Lys Glu Gln Lys
 165 170 175
 Thr Ala His Phe Leu Pro Met Ala Ile Thr
 180 185

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATGTGCAAT GACATGACTC CAGAGCAAAT GGCTACAAAT GTGAACTGTT CCAGCCCTGA 60
 GCGACACACA AGAAGTTATG ATTACATGGA AGGAGGGGAT ATAAGAGTGA GAAGACTCTT 120
 CTGTGGAACA CAGTGGTACC TGAGGATCGA TAAAGAGGCC AAAGTAAAAG GGACCCAAGA 180

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GATGAAGAAT AATTACAATA TCATGGAAAT CAGGACAGTG GCAGTTGGAA TTGTGGCAAT 240
 CAAAGGGGTG GAAAGTGAAT TCTATCTTGC AATGAACAAG GAAGGAAAAC TCTATGCAAA 300
 GAAAGAATGC AATGAAGATT GTAACCTCAA AGAACTAATT CTGGAAAACC ATTACAACAC 360
 ATATGCATCA GCTAAATGGA CACACAACGG AGGGGAAATG TTTGTTGCCT TAAATCAAAA 420
 GGGGATTCCCT GTAAGAGGAA AAAAAACGAA GAAAGAACAA AAAACAGCCC ACTTTCTTCC 480
 TATGGCAATA ACTTAATAG 499

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Cys	Asn	Asp	Met	Thr	Pro	Glu	Gln	Met	Ala	Thr	Asn	Val	Asn	Cys	1	5	10	15
Ser	Ser	Pro	Glu	Arg	His	Thr	Arg	Ser	Tyr	Asp	Tyr	Met	Glu	Gly	Gly	20	25	30	
Asp	Ile	Arg	Val	Arg	Arg	Leu	Phe	Cys	Arg	Thr	Gln	Trp	Tyr	Leu	Arg	35	40	45	
Ile	Asp	Lys	Arg	Gly	Lys	Val	Lys	Gly	Thr	Gln	Glu	Met	Lys	Asn	Asn	50	55	60	
Tyr	Asn	Ile	Met	Glu	Ile	Arg	Thr	Val	Ala	Val	Gly	Ile	Val	Ala	Ile	65	70	75	80
Lys	Gly	Val	Glu	Ser	Glu	Phe	Tyr	Leu	Ala	Met	Asn	Lys	Glu	Gly	Lys	85	90	95	
Leu	Tyr	Ala	Lys	Lys	Glu	Cys	Asn	Glu	Asp	Cys	Asn	Phe	Lys	Glu	Leu	100	105	110	
Ile	Leu	Glu	Asn	His	Tyr	Asn	Thr	Tyr	Ala	Ser	Ala	Lys	Trp	Thr	His	115	120	125	
Asn	Gly	Gly	Glu	Met	Phe	Val	Ala	Leu	Asn	Gln	Lys	Gly	Ile	Pro	Val	130	135	140	
Arg	Gly	Lys	Lys	Thr	Lys	Lys	Glu	Gln	Lys	Thr	Ala	His	Phe	Leu	Pro	145	150	155	160
Met	Ala	Ile	Thr																

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAATGACCTA GGAGTAACAA TCAAC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAAACAAACA TAAATGCACA AGTCCA

26

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACAACGCGTG CAATGACATG ACTCCA

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACAGGATCCT ATTAAGTTAT TGCCATAGGA A

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACACATATGT GCAATGACAT GACTCCA

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGCGTATCG ACAAACGCGG CAAAGTCAAG GGCACCC

37

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGAGATGAA AAACAACCTAC AATATTATGG AAATCCGTAC TGTT

44

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGTTGGTA TCGTTGCAAT CAAAGGTGTT GAATCTG

37

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTTGGGTGC CCTTGACTTT GCCGCGTTTG TCGATACGCA GGTAC

45

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACAGCAACAG TACGGATTTC CATAATATTG TAGTTGTTTT TCATC

45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AATTCAGATT CAACACCTTT GATTGCAACG ATACCA

36

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTTTTGATC TAGAAGGAGG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCAAAACTGG ATCCTATTAA

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGTTTTGATC TAGAAGGAGG AATAACATAT GTGCAACGAC ATGACTCCGG AACAGATGGC

60

TACCAACGTT AACTGCTCCA GCCCGGAACG T

91

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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACACCCGTA GCTACGACTA CATGGAAGGT GGTGACATCC GTGTCGTCG TCTGTTCTGC 60
CGTACCCAGT GGTACCTGCG TATCGACAAA 90

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTGGTAAAG TTAAAGGTAC CCAGGAAATG AAAACAACACT ACAACATCAT GGAAATCCGT 60
ACTGTTGCTG TTGGTATCGT TGCAATCAAA 90

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTGTGAAT CTGAATTCTA CCTGGCAATG AACAAAGAAG GTAAACTGTA CGCAAAAAAA 60
GAATGCAACG AAGACTGCAA CTTCAAAGAA 90

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGATCCTGG AAAACCACTA CAACACCTAC GCATCTGCTA AATGGACCCA CAACGGTGGT 60
GAAATGTTTCG TTGCTCTGAA CCAGAAAGGT 90

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCCCGGTTTC GTGGTAAAAA AACCAAAAAA GAACAGAAAA CCGCTCACTT CCTGCCGATG 60
GCAATCACTT AATAGGATCC AGTTTTGA 88

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TACGGGTGTG ACGTTCGGG 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTTTACCACG TTTGTCGATA

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATTCAACACC TTTGATTGCA

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAGGATCAG TTCTTTGAAG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAACCGGGAT ACCTTCTGG

20

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

ATGTCTAATG ATATGACTCC GGAACAGATG GCTACCAACG TTAACTCCTC CTCCCCGGAA      60
CGTCACACGC GTTCCTACGA CTACATGGAA GGTGGTGACA TCCGCGTACG TCGTCTGTTC      120
TGCCGTACCC AGTGGTACCT GCGTATCGAC AAACGCGGCA AAGTCAAGGG CACCCAAGAG      180
ATGAAAAACA ACTACAATAT TATGGAAATC CGTACTGTTG CTGTTGGTAT CGTTGCAATC      240
AAAGGTGTTG AATCTGAATT CTACCTGGCA ATGAACAAAG AAGGTAACT GTACGCAAAA      300
AAAGAATGCA ACGAAGACTG CAACTTCAAA GAACTGATCC TGGAAAACCA CTACAACACC      360
TACGCATCTG CTAAATGGAC CCACAACGGT GGTGAAATGT TCGTTGCTCT GAACCAGAAA      420
GGTATCCCCG TTCGTGGTAA AAAAACCAAA AAAGAACAGA AAACCGCTCA CTTCTGCCG      480
ATGGCAATCA CTTAA                                         495

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Ser Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Ser
1           5           10
Ser Ser Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly
20          25          30
Asp Ile Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg
35          40          45
Ile Asp Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn
50          55          60

```

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Tyr Asn Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile
 65 70 75 80
 Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys
 85 90 95
 Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu
 100 105 110
 Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His
 115 120 125
 Asn Gly Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val
 130 135 140
 Arg Gly Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro
 145 150 155 160
 Met Ala Ile Thr

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAATG ATATGACTCC TGAACAAATG GCTACCAATG TCAACTGTTC CTCTCCGGAG 60
 CGCCACACCC GGAGTTACGA TTACATGGAA GGTGGGGATA TTCGCGTACG TCGTCTGTTC 120
 TGCCGTACCC AGTGGTACCT GCGTATCGAC AAACGCGGCA AAGTCAAGGG CACCCAAGAG 180
 ATGAAAAACA ACTACAATAT TATGGAAATC CGTACTGTTG CTGTGTTGAT CGTTGCAATC 240
 AAAGGTGTTG AATCTGAATT CTATCTTGCA ATGAACAAGG AAGGAAAACCT CTATGCAAAG 300
 AAAGAATGCA ATGAAGATTG TAACTTCAAA GAACTAATTC TGGAAAACCA TTACAACACA 360
 TATGCATCTG CTAAATGGAC CCACAACGGT GGTGAAATGT TCGTTGCTCT GAACCAGAAA 420
 GGTATCCCTG TTCAAGGTAA GAAAACCAAG AAAGAACAGA AAACCGCTCA CTTCTGCCG 480
 ATGGCAATCA CTAA 495

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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Cys Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys
1          5          10          15

Ser Ser Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly
          20          25          30

Asp Ile Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg
          35          40          45

Ile Asp Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn
50          55          60

Tyr Asn Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile
65          70          75          80

Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys
          85          90          95

Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu
          100          105          110

Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His
          115          120          125

Asn Gly Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val
          130          135          140

Gln Gly Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro
145          150          155          160

Met Ala Ile Thr

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

ATGTCTAATG ATATGACTCC GGAACAGATG GCTACCAACG TTAACCTCTC CTCCCCGGAA      60
CGTCACACGC GTTCCTACGA CTACATGGAA GGTGGTGACA TCCGCGTACG TCGTCTGTTC      120
TGCCGTACCC AGTGGTACCT GCGTATCGAC AAACGCGGCA AAGTCAAGGG CACCCAAGAG      180
ATGAAAAACA ACTACAATAT TATGGAAATC CGTACTGTTG CTGTTGGTAT CGTTGCAATC      240
AAAGGTGTTG AATCTGAATT CTATCTTGCA ATGAACAAGG AAGGAAAACT CTATGCAAAG      300
AAAGAATGCA ATGAAGATTG TAACTTCAAA GAACATAATC TGGAAAACCA TTACAACACA      360
TATGCATCTG CTAAATGGAC CCACAACGGT GGTGAAATGT TCGTTGCTCT GAACCAGAAA      420
GGTATCCCTG TTCAAGGTAA GAAAACCAAG AAAGAACAGA AAACCGCTCA CTTCTGCCG      480
ATGGCAATCA CTAA                                     495

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Ser Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Ser
1      5      10
Ser Ser Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly
20     25     30
Asp Ile Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg
35     40     45
Ile Asp Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn
50     55     60
Tyr Asn Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile
65     70     75     80
Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys
85     90     95
Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu
100    105    110
Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His
115    120    125

```

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Asn Gly Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val
 130 135 140

Gln Gly Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro
 145 150 155 160

Met Ala Ile Thr

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGTCTTCTC CTGAACGTCA TACGCGTTCC TACGACTACA TGGAAGGTGG TGACATCCGC	60
GTACGTCGTC TGTTCGTCCG TACCCAGTGG TACCTGCGTA TCGACAAACG CGGCAAAGTC	120
AAGGGCACCC AAGAGATGAA AAACAACCTAC AATATTATGG AAATCCGTAC TGTTGCTGTT	180
GGTATCGTTG CAATCAAAGG TGTGAATCT GAATTCTACC TGGCAATGAA CAAAGAAGGT	240
AAACTGTACG CAAAAAAGA ATGCAACGAA GACTGCAACT TCAAAGAACT GATCCTGGAA	300
AACCACTACA ACACCTACGC ATCTGCTAAA TGGACCCACA ACGGTGGTGA AATGTTCGTT	360
GCTCTGAACC AGAAAGGTAT CCCGGTTCGT GGTAAAAAAA CCAAAAAAGA ACAGAAAACC	420
GCTCACTTCC TGCCGATGGC AATCACTTAA	450

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ser Ser Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly	
1 5 10 15	
Gly Asp Ile Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu	
20 25 30	

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Arg Ile Asp Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn
 35 40 45
 Asn Tyr Asn Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala
 50 55 60
 Ile Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly
 65 70 75 80
 Lys Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu
 85 90 95
 Leu Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr
 100 105 110
 His Asn Gly Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro
 115 120 125
 Val Arg Gly Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu
 130 135 140
 Pro Met Ala Ile Thr
 145

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGTCCTACG ACTACATGGA AGGTGGTGAC ATCCGCGTAC GTCGTCTGTT CTGCCGTACC	60
CAGTGGTACC TCGTATCGA CAAACGCGGC AAAGTCAAGG GCACCCAAGA GATGAAAAAC	120
AACTACAATA TTATGGAAAT CCGTACTGTT GCTGTGGTA TCGTTGCAAT CAAAGGTGTT	180
GAATCTGAAT TCTACCTGGC AATGAACAAA GAAGGTAAAC TGTACGCAAA AAAAGAATGC	240
AACGAAGACT GCAACTTCAA AGAAGTGATC CTGGAAAACC ACTACAACAC CTACGCATCT	300
GCTAAATGGA CCCACAACGG TGGTGAAATG TTCGTGCTC TGAACCAGAA AGGTATCCCG	360
GTTCTGGTA AAAAAACCAA AAAAGAACAG AAAACGCTC ACTTCCTGCC GATGGCAATC	420
ACTTAA	426

- 48 -

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Met Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg Arg Leu
1           5           10           15
Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp Lys Arg Gly Lys Val
                20           25           30
Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn Ile Met Glu Ile Arg
                35           40           45
Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly Val Glu Ser Glu Phe
                50           55           60
Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr Ala Lys Lys Glu Cys
65           70           75           80
Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu Glu Asn His Tyr Asn
                85           90           95
Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly Gly Glu Met Phe Val
                100          105          110
Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly Lys Lys Thr Lys Lys
                115          120          125
Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala Ile Thr
                130          135          140

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

ATGTCCTACG ACTACATGGA AGGTGGTGAC ATCCGCGTAC GTCGTCTGTT CTGCCGTACC      60
CAGTGGTACC TGCCTATCGA CAAACGCGGC AAAGTCAAGG GCACCCAAGA GATGAAAAAC      120
AACTACAATA TTATGGAAAT CCGTACTGTT GCTGTTGGTA TCGTTGCAAT CAAAGGTGTT      180
GAATCTGAAT TCTATCTTGC AATGAACAAG GAAGGAAAAC TCTATGCAA GAAAGAATGC      240
AATGAAGATT GTAACCTCAA AGAACTAATT CTGGAAAACC ATTACAACAC ATATGCATCT      300
GCTAAATGGA CCCACAACGG TGGTGAAATG TTCGTTGCTC TGAACCAGAA AGGTATCCCT      360
GTTCAAGGTA AGAAAACCAA GAAAGAACAG AAAACCGCTC ACTTCCTGCC GATGGCAATC      420
ACTTAA                                         426

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg Arg Leu
 1           5           10           15
Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp Lys Arg Gly Lys Val
 20           25           30
Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn Ile Met Glu Ile Arg
 35           40           45
Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly Val Glu Ser Glu Phe
 50           55           60
Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr Ala Lys Lys Glu Cys
 65           70           75           80
Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu Glu Asn His Tyr Asn
 85           90           95
Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly Gly Glu Met Phe Val
100          105          110
Ala Leu Asn Gln Lys Gly Ile Pro Val Gln Gly Lys Lys Thr Lys Lys
115          120          125
Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala Ile Thr
130          135          140

```

- 50 -

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAGCTCACTA GTGTCGACCT GCAG

24

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: complement (1..24)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTGCAGGTCG AACTAGTGA GCTC

24

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAATCTACAA TTCACAGA

18

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid

- 51 -

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTAAGTTATT GCCATAGG

18

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AACAAAGCTT CTACAATTCA CAGATAGGA

29

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACAAGATCT TAAGTTATTG CCATAGG

27

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGTCTAGAC CACCATGCAC AAATGGATAC TGACATGG

38

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(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCGTCGACC TATTAAGTTA TTGCCATAGG AAG

33

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Xaa	Asn	Asp	Met	Thr	Pro	Glu	Gln	Met	Ala	Thr	Asn	Val	Xaa	Xaa	Ser
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser	Tyr	Asp	Tyr	Met	Glu	Gly	Gly	Asp	Ile	Arg	Val
1				5				10			

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WHAT IS CLAIMED IS:

1. A method for purifying a keratinocyte growth factor (KGF), the method comprising:
 - 5 a) obtaining a solution comprising KGF;
 - b) binding KGF from the solution of part (a) to a cation exchange resin;
 - c) eluting KGF in an eluate solution from the cation exchange resin;
 - 10 d) passing the eluate solution from part (c) through an appropriate molecular weight exclusion matrix; and
 - e) recovering KGF from the molecular weight exclusion matrix.
- 15 2. The method according to Claim 1 wherein the KGF is produced in procaryotic cells.
3. The method according to Claim 1 wherein the
20 KGF is produced in *E. coli*.
4. The method according to Claim 1 wherein the KGF is produced in mammalian cells.
- 25 5. The method according to Claim 4 wherein the KGF is produced in Chinese hamster ovary cells.
6. A method for purifying a keratinocyte growth factor (KGF), the method comprising:
 - 30 a) obtaining a solution comprising KGF;
 - b) binding KGF from the solution of part (a) to a cation exchange resin;
 - c) eluting KGF in an eluate solution from the cation exchange resin;

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- d) performing hydrophobic interaction chromatography on the eluate solution of part (c); and
- e) recovering KGF from the hydrophobic interaction chromatography step of part (d).

5

7. A method according to Claim 6 further comprising oxidation of free sulfhydryl groups in KGF.

10

8. The method according to Claim 6 wherein the KGF is produced in procaryotic cells.

9. The method according to Claim 7 wherein the KGF is produced in *E. coli*.

15

10. The method according to Claim 6 wherein the KGF is produced in mammalian cells.

11. The method according to Claim 10 wherein the KGF is produced in Chinese hamster ovary cells.

20

Figure 1

human KGF (+ signal sequence)

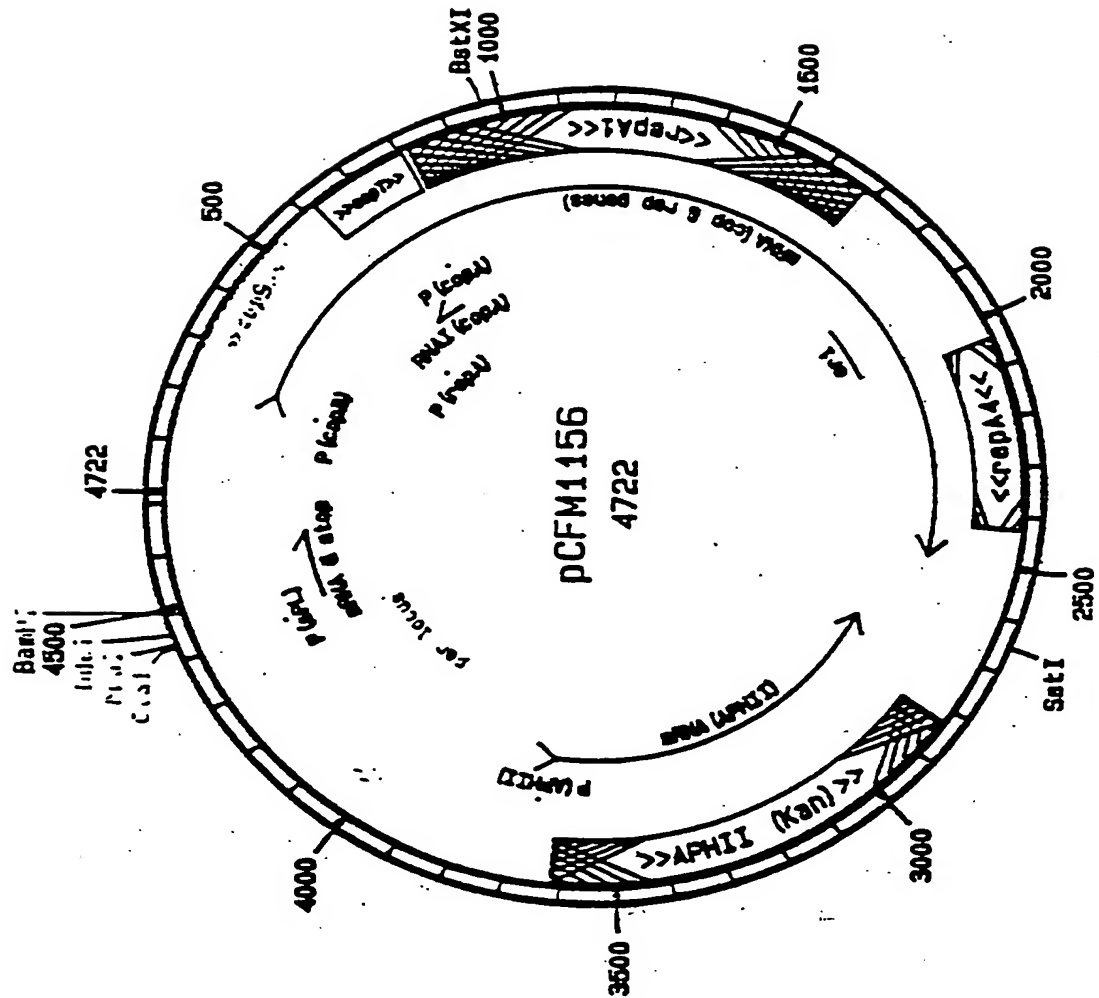
|-----OLIGO#25-----| |-----OLIGO#1-----|
 5'CAATCTACAATTCACAGA 3' 5'CAATGACCTAGGAGTAACAATCAAC 3'
 5'CAATCTACAATTCACAGATAGGAAGAGGTCATGACCTAGGAGTAACAATCAACTCAAGA-
 ----- 60
 -TTCATTTTCATTATGTTATTTCATGAACACCCGGAGCACTACACTATAATGCACAAATGGA-
 ----- 120
 M H K W I
 -TACTGACATGGATCCTGCCAACTTTGCTGTACAGATCATGCTTTCACATTATCTGTCTAG-
 ----- 180
 L T W I L P T L L Y R S C F H I I C L V
 -TGGGTACTATATCTTTAGCTTGCAATGACATGACTCCAGAGCAATGGCTACAAATGTGA-
 ----- 240
 G T I S L A C N D M T P E Q M A T N V N
 -ACTGTCCAGCCCTGAGCGACACACAAGAAGTTATGATTACATGGAAGGAGGGGATATAA-
 ----- 300
 C S S P E R H T R S Y D Y M E G G D I R
 -GAGTGAGAAGACTCTTCTGTGCGAACACAGTGGTACCTGAGGATCGATAAAGAGGCCAAG-
 ----- 360
 V R R L F C R T Q W Y L R I D K R G K V
 -TAAAGGGGACCCAGAGATGAAGAATAATTACAATATCATGGAATCAGGACAGTGGCAG-
 ----- 420
 K G T Q E M K N N Y N I M E I R T V A V
 -TTGGAATTGTGGCAATCAAGGGGTGGAAAGTGAATTCTATCTTGCAATGAACAAGGAAG-
 ----- 480
 G I V A I K G V E S E F Y L A M N K E G
 -GAAACTCTATGCAAGAAAGAATGCAATGAAGATTGTAACCTCAAGAAGTAATTCTGG-
 ----- 540
 K L Y A K K E C N E D C N F K E L I L E
 -AAAACCATTAACACATATGCATCAGCTAAATGGACACACACGGAGGGGAAATGTTTG-
 ----- 600
 N H Y N T Y A S A K W T H N G G E M F V
 -TTGCCTTAAATCAAGGGGATTCTCTGTAAGAGGAAAAAACGAAGAAAGAACAAAAA-
 ----- 660
 A L N Q K G I P V R G K K T K K E Q K T
 -CAGCCCACTTCTCTCTATGGCAATAACTTAATTGCATATGGTATATAAAGAACCCAGTT
 ----- 720
 A H F L P M A I T *
 3'GGATACCGTTATTGAATT 5'
 |-----OLIGO#25-----| :

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(continued)

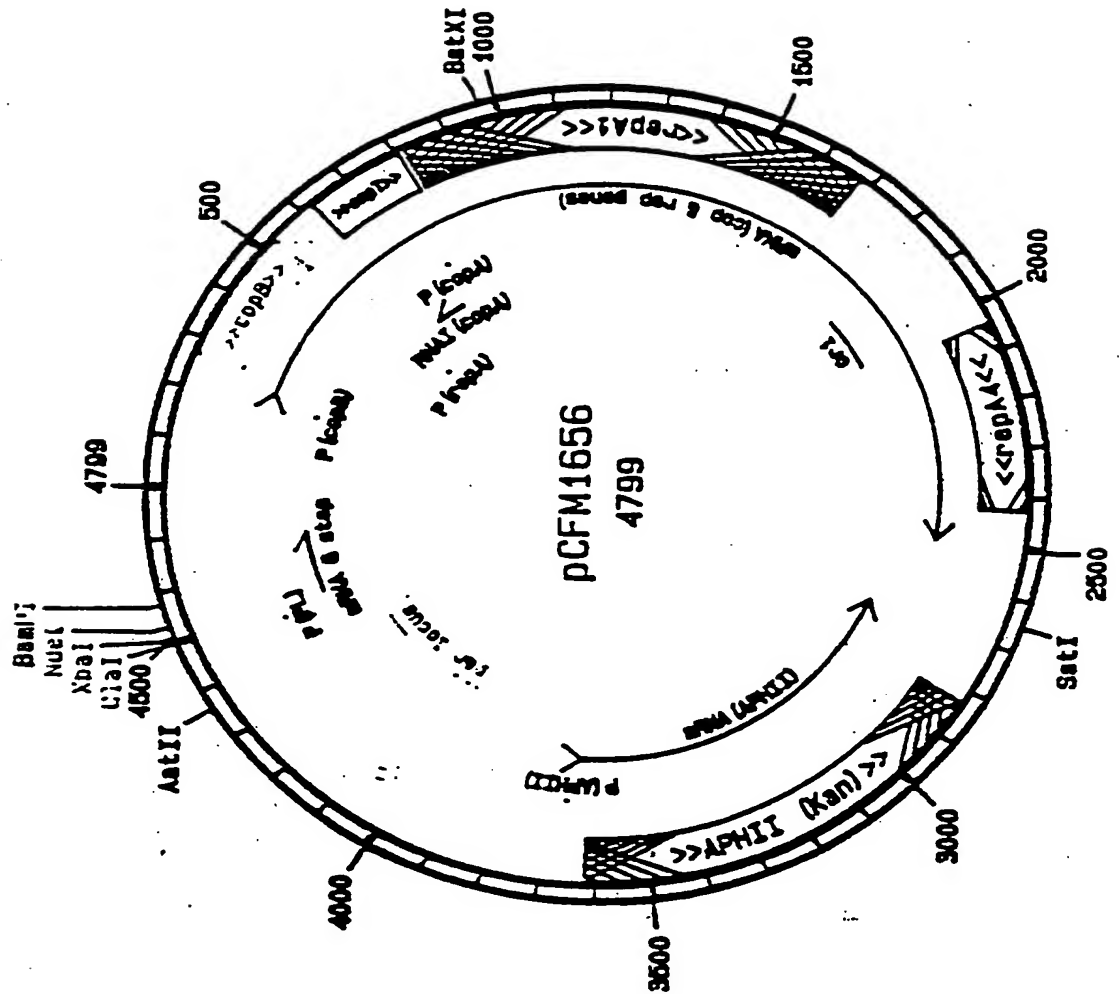
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-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780

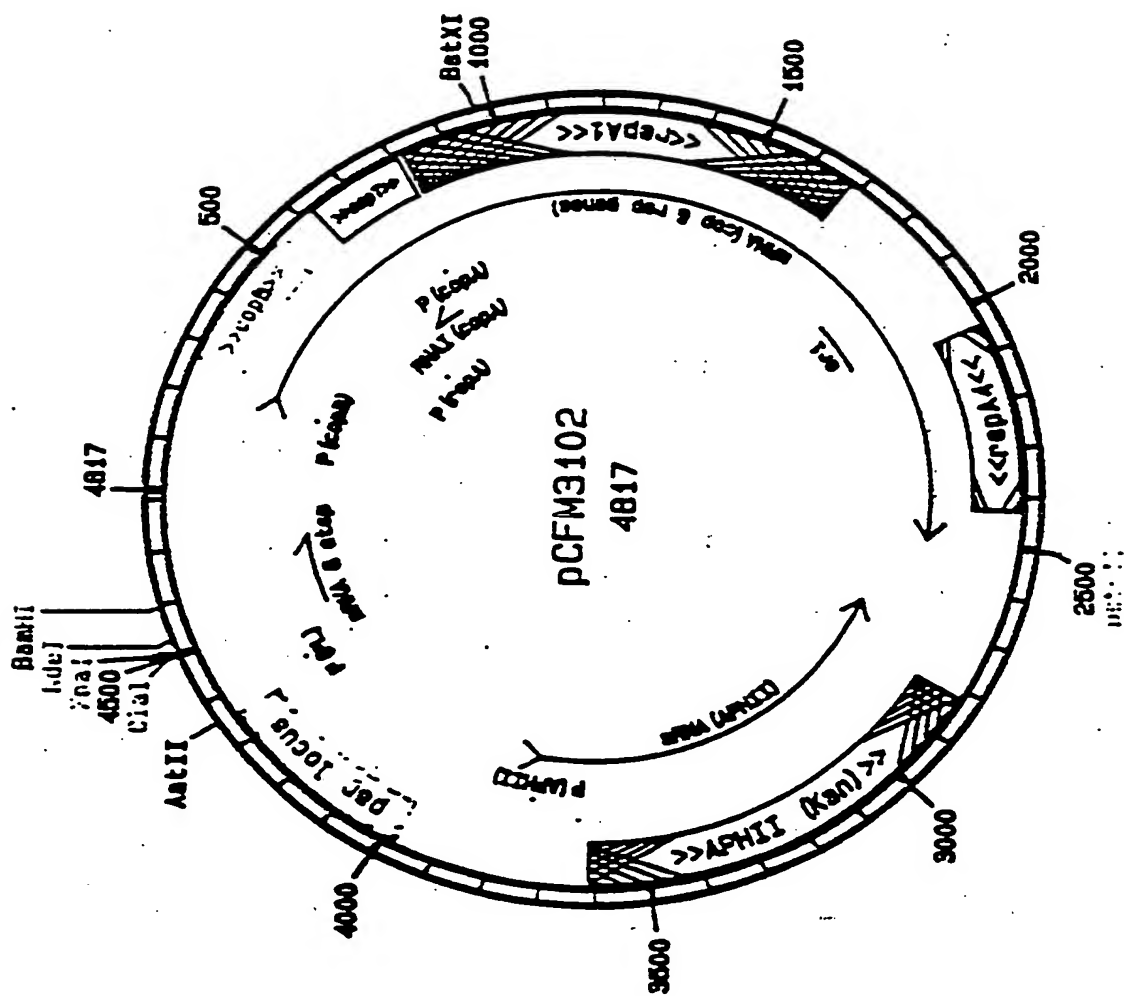
-TATTTTTTAGTAATCAAGAAAGGCTGGAAAACTACTGAAAACTGATCAAGCTGGACTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
3'ACCTGAA-
|-----

-GTGCATTATGTTTGTTTTAAG 3'
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 862
-CACGTAATACAAACAAA 3'
---OLIGO#2-----|



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RSB-KGE

ClaI
XbaI
NdeI
 5'-ATCGATTGATTCTAGAAGGAGGAATACATATGAAAG-
M K K

RSH signal sequence MluI
 -CGCGCACGTGCTATCGCCATTGCTGTGGCTCTGGCAGGTTTCGCACTAGTGCACA-3'
 R A R A I A I A V A L A G F A T S A H A

MluI
5' CGCGTGAATGACATGACTCCAGAGCAATGGCTACAAATGTGAAGTGTTCAGCCCTGA-
- C N D M T P E Q M A T N V N C S S P E 60

-GCGACACACAGAAGTTATGATTACATGGAAGGAGGGGATATAAGAGTGAGAAGACTCTT-
 R H T R S Y D Y M E G G D I R V R R L F 120

KpnI ClaI
 -CTGTCGAACACAGTGGTACCTGAGGATCGATAAAAGAGGCCAAAGTAAAGGGGACCCAAGA-
 C R T Q W Y L R I D K R G K V K G T Q E 180

-GATGAAGAATAATTACATATCATGGAAATCAGGACAGTGGCAGTTGGAATTTGTGGCAAT- 240
M K N N Y N I M E I R T V A V G I V A I

EcoRI

-CAAAGGGGTGGAAAGTGAATTCATCTTGCATGAACAAGGAAGGAAACTCTATGCAA-

300

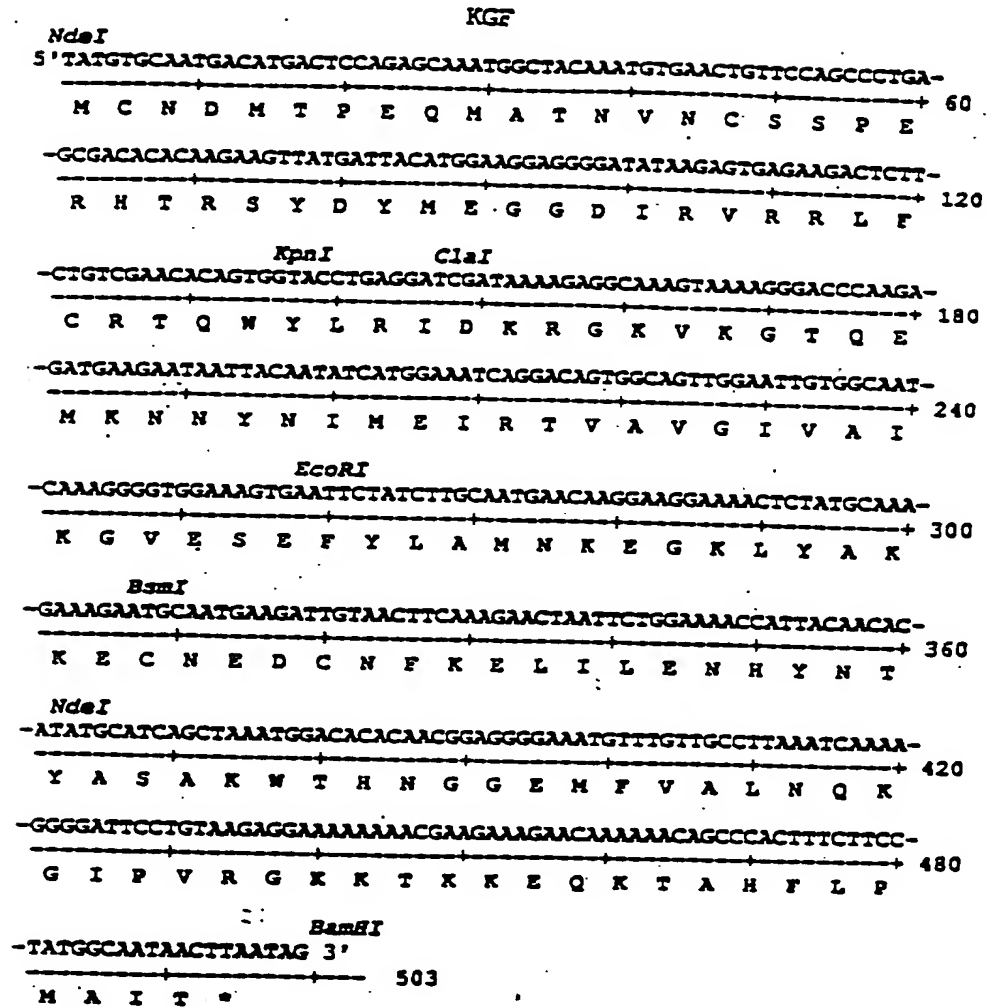
K G V E S E F Y L A M N K E G K L Y A K

BsmI
 -GAAGATGCAATGAAGATTGTAACCTTCAGAACTAATCTGGAAACCATTAACAC-
 K E C N E D C N F K E L I L E N H Y N T 360

NdeI
-ATATGCATCAGTAAATGGACACACACGGAGGGGAATGTTTGTTCCTTAAATCAAA-
Y A S A K W T H N G G E M F V A L N Q K 420

[illegible]

^{BamHI}
 -TATGGCAATAACTTAATAG 3'
 ----- 503
 M A I T * * -plasmid DNA
 -sequence

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Figure 4

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Figure 5

substitution of KpnI to EcoRI sequence to make KGF(dsd)



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Figure 6

KGF (codon optimized)

XbaI
 |-----OLIGO#12-----|
 5' AGTTTGTGATCTAGAAGGAGG 3'
 |-----OLIGO#14-----|
 5' AGTTTGTGATCTAGAAGGAGGAATAACATATGTGCAACGACATGACTCCGGAACAGATGGCT-
 |-----OLIGO#15-----|
 -ACCAACGTTAACTGCTCCAGCCCGGAACGTCACACCCGTAGCTACGACTACATGGAAGGTG-
 3' GGGCCTTGCAGTGTGGGCAT 5'
 |-----OLIGO#20-----|
 |-----OLIGO#15-----|
 -GTGACATCCGTGTTCTGTCGTCTGTTCTGCCGTACCCAGTGGTACCTGCGTATCGACAAACG-
 3' ATAGCTGTTTGC-
 |-----OLIGO#21-----|
 |-----OLIGO#16-----|
 -TGGTAAAGTTAAAGGTACCCAGGAAATGAAAAACAACCTACAACATCATGGAAATCCGTACT-
 -ACCATTTT 5'
 |-----OLIGO#17-----|
 -GTTGCTGTGGTATCGTTGCAATCAAGGTGTTGAATCTGAATCTACCTGGCAATGAACA-
 3' ACGTTAGTTTCCACAACCTA 5'
 |-----OLIGO#22-----|
 |-----OLIGO#17-----|
 -AAGAAGGTAACTGTACGCAAAAAAAGAAATGCAACGAAGACTGCAACTTCAAGAAGTAT-
 3' GAAGTTTCTTGACTA-
 |-----OLIGO#23-----|
 |-----OLIGO#18-----|
 -CCTGGAAGAAACCACTACACACCTACGCATCTGCTAAATGGACCCACACGGTGGTGAAATG-
 -GGACC 5'
 |-----OLIGO#19-----|
 -TTCGTTGCTCTGAACCAAGGTATCCCGGTTCTGTTGTTAAAAAACCAGAAAGAACAGA-
 3' GGTCTTTCCATAGGGCCAG 5'
 |-----OLIGO#24-----|
 |-----OLIGO#19-----|
 -AAACCGCTCACTTCTGCGGATGGCAATCACTTAATAGGATCCAGTTTGA 3'
 3' AATTATCCTAGGTCAAACT 5'
 |-----OLIGO#13-----|
 BamHI

Figure 7

KGF C(1,15)S

5' ATGTCTAATGATATGACTCCGGAACAGATGGCTACCAACGTTAACTCCTCCTCCCGGAA-
M S N D M T P E Q M A T N V N S S S P E 60
-CGTCACACGCGTTCCTACGACTACATGGAAGGTGGTGACATCCGCGTACGTCGTCGTTC-
R H T R S Y D Y M E G G D I R V R R L F 120
-TGCCGTACCCAGTGGTACCTGCGTATCGACAAACGGCGCAAGTCAAGGGCACCCAGAG-
C R T Q W Y L R I D K R G K V K G T Q E 180
-ATGAAAAACAACTACAATATTATGGAAATCCGTACTGTTGCTGTTGGTATCGTTGCAATC-
M K N N Y N I M E I R T V A V G I V A I 240
-AAAGGTGTTGAATCTGAATTCTACCTGGCAATGAACAAAGAAGGTAACTGTACGCAAAA-
K G V E S E F Y L A M N K E G K L Y A K 300
-AAAGAATGCAACGAAGACTGCAACTTCAAGAAGTATCCTGGAAAACCACTACAACACC-
K E C N E D C N F K E L I L E N H Y N T 360
-TACGCATCTGCTAAATGGACCCACAACGGTGGTGAAATGTTGCTGCTGAACCAAGAAA-
Y A S A K W T H N G G E M F V A L N Q K 420
-GGTATCCCGGTTGTTGGTAAAAAAACCAAAAAAGAACAGAAAACCGCTCACTTCCTGCCG-
G I P V R G K K T K K E Q K T A H F L P 480
-ATGGCAATCACTTAA 3' 495
M A I T *

11/15
Figure 8
KGF R(144)Q

5' ATGTGCAATGATATGACTCCTGAACAAATGGCTACCAATGTCAACTGTTCTCTCCGGAG-
M C N D M T P E Q M A T N V N C S S P E 60
-CGCCACACCCGGAGTTACGATTACATGGAAGGTGGGATATTCCGGTACGTCGTCGTTC-
R H T R S Y D Y M E G G D I R V R R L F 120
-TGCCGTACCCAGTGGTACCTGCGTATCGACAAACGCGGCAAAGTCAAGGGCACCCAAAGAG-
C R T Q W Y L R I D K R G K V K G T Q E 180
-ATGAAAACAACACTACAATATTATGGAATCCGTAAGTGTGCTGTGGTATCGTTGCAATC-
M K N N Y N I M E I R T V A V G I V A I 240
-AAAGGTGTTGAATCTGAATTCATCTTGAATGAACAAGGAAGGAAAACCTCTATGCAAG-
K G V E S E F Y L A M N K E G K L Y A K 300
-AAAGAATGCAATGAAGATTGTAACCTCAAGAAGTAATTCGGAAGAACATTACAACACA-
K E C N E D C N F K E L I L E N H Y N T 360
-TATGCATCTGCTAAATGGACCCACAACGGTGGTGAATGTTCTGCTCTGAACCAGAAA-
Y A S A K W T H N G G E M F V A L N Q K 420
-GGTATCCCTGTTCAAGGTAAGAAAACCAAGAAAGAACAGAAAACCGCTCACTTCCTGCCG-
G I P V Q G K K T K K E Q K T A H F L P 480
-ATGGCAATCACTTAA 3'
495
M A I T *

12/15

Figure 9

KGF C(1,15)S/R(144)Q

5' ATGTCCTAATGATATGACTCCGGAAACAGATGGCTACCAACGTTAACTCCTCCTCCCGGAA- 60
M S N D M T P E Q M A T N V N S S S P E
-CGTCACACGCGTTCCTACGACTACATGGAAGGTGGTGACATCCGCGTACGTCGTCTGTT- 120
R H T R S Y D Y M E G G D I R V R R L F
-TGCCGTACCCAGTGGTACCTGCGTATCGACAAACGCGGCAAGTCAAGGGCACCCAAAG- 180
C R T Q W Y L R I D K R G K V K G T Q E
-ATGAAAACAACACTACAATATTATGGAATCCGTACTGTTGCTGTTGGTATCGTTGCAATC- 240
M K N N Y N I M E I R T V A V G I V A I
-AAAGGTGTTGAATCTGAATTCTATCTTGCATGAACAAGGAAGGAAACTCTATGCAAG- 300
K G V E S E F Y L A M N K E G K L Y A K
-AAAGAATGCAATGAAGATTGTAACCTCAAAGAAGTAACTCTGGAAAACCATTAACACA- 360
K E C N E D C N F K E L I L E N H Y N T
-TATGCATCTGCTAAATGGACCCACACGCGTGGTGAAATGTTGCTGCTCTGAACCAGAAA- 420
Y A S A K W T H N G G E M F V A L N Q K
-GGTATCCCTGTTCAAGGTAAAGAAAACCAAGAAAGAACAGAAAACCGCTCACTTCCTGCGG- 480
G I P V Q G K K T K K E Q K T A H F L P
-ATGGCAATCACTTAA 3' 495
M A I T *

13/15

Figure 10
KGF ΔN15

5' ATGTCCTCTCTGAACTGATACCGGTTCTACGACTACATGGAAGGTGGTGACATCCGC-
M S S P E R H T R S Y D Y M E G G D I R 60
-GTACGTCGTCTGTCTGCGGTACCCAGTGGTACCTGCGTATCGACAAACGCGGCAAGTC-
V R R L F C R T Q W Y L R I D K R G K V 120
-AAGGGCACCCAGAGATGAAAACAACCTACATATTATGGAATCCGTACTGTTGCTGTT-
K G T Q E M K N N Y N I M E I R T V A V 180
-GGTATCGTTGCAATCAAGGTGTTGAATCTGAATTCTACCTGGCAATGAACAAGAAGGT-
G I V A I K G V E S E F Y L A M N K E G 240
-AAACTGTACGCAAAAAAGAAATGCAACGAAGACTGCAACTTCAAAGAAGTATCCTGGAA-
K L Y A K K E C N E D C N F K E L I L E 300
-AACCCTACAAACACCTACGCATCTGCTAAATGGACCCACAACGGTGGTGAATGTTCTGTT-
N H Y N T Y A S A K W T E N G G E M F V 360
-GCTCTGAACCAAGGATATCCCGGTTCTGGTAAAAAACCAGAAAGAACAGAAACC-
A L N Q K G I P V R G K K T K K E Q K T 420
-GCTCACTTCTGCGGATGGCAATCACTTAA 3' 450
A H F L P M A I T *

Figure 11.

KGF ΔN23

5' ATGTCCTACGACTACATGGAAGGTGGTGACATCCGCGTACGTCGTCTGTTCTGCCGTACC-
M S Y D Y M E G G D I R V R R L F C R T 60
-CAGTGGTACCTGCGTATCGACAAACGCGGCAAGTCAAGGGCACCCAGAGATGAAAAAC-
Q W Y L R I D K R G K V K G T Q E M K N 120
-AACTACAATATTATGGAATCCGTACTGTTGCTGTTGGTATCGTTGCAATCAAGGTGTT-
N Y N I M E I R T V A V G I V A I K G V 180
-GAATCTGAATTCTACCTGGCAATGAACAAAGAAGGTAACTGTACGCAAAAAAGAATGC-
E S E F Y L A M N K E G K L Y A K K E C 240
-AACGAAGACTGCAACTCAAGAAGTGTATCCTGGAAAACCACTACAACACCTACGCATCT-
N E D C N F K E L I L E N H Y N T Y A S 300
-GCTAAATGGACCCACAACGGTGGTGAATGTTGCTGCTGTAACCAGAAAGGTATCCCG -
A K N T H N G G E M F V A L N Q K G I P 360
-GTTCGTGGTAAAAAACCAGAAAGAACAGAAACCGCTCACTTCCTGCGGATGGCAATC-
V R G K K T K K E Q K T A H F L P M A I 420
-ACTTAA 3'
426
T *

Figure 12

KGF ΔN23/R(144)Q

5' ATGTCTACGACTACATGGAAGGTGGTGACATCCCGGTACGTCGTCGTCTGTTCTGCCGTACC-
M S Y D Y M E G G D I R V R R L F C R T 60
-CAGTGGTACCTGCGTATCGACAAACGCGGCAAGTCAAGGGCACCCAAGAGATGAAAAAC-
Q W Y L R I D K R G K V K G T Q E M K N 120
-AACTACAATATTATGGAAATCCGTACTGTTGCTGTTGGTATCGTTGCAATCAAAGGTGTT-
N Y N I M E I R T V A V G I V A I K G V 180
-GAATCTGAATTCTATCTTGCATGAACAAGGAAGGAAAACCTCTATGCAAGAAAGAATGC-
E S E F Y L A M N K E G K L Y A K K E C 240
-AATGAAGATTGTAACCTTCAAAGAACTAATTCTGGAAAACCATTAACACATATGCATCT-
N E D C N F K E L I L E N H Y N T Y A S 300
-GCTAAATGGACCCACAACGGTGGTGAATGTTTCGTTGCTCTGAACCAGAAAGGTATCCCT-
A K W T H N G G E M F V A L N Q K G I P 360
-GTCAAGGTAAAGAAACCAAGAAAGAACAGAAAACCGCTCACTTCTGCGGATGGCAATC-
V Q G K K T K K E Q K T A H F L P M A I 420
-ACTTAA 3'
426
T *

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/13899

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C07K14/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	FEBS LETTERS, vol. 328, no. 1,2, - August 1993 AMSTERDAM NL, pages 17-20, M.SUZUKI E A 'Spleen-derived growth factor, SDGF-3, is identified as keratinocyte growth factor (KGF)' see page 18	1-5
A	--- JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 268, no. 4, 5 February 1993 MD US, pages 2984-2988, D. RON ET AL 'Expression of biologically active recombinant KGF' cited in the application see the whole document --- -/-	1-11

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

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Date of the actual completion of the international search

28 February 1996

Date of mailing of the international search report

15. 03 96

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Groenendijk, M

INTERNATIONAL SEARCH REPORT

International Application No

PC7/US 95/13899

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO, A, 98 08771 (RUBIN JEFFREY S ;FINCH PAUL W (US); AARONSON STUART A (US)) 9 August 1998 cited in the application The whole document; see especially p.13, lines 2-7, p.40 to 43; page 66, lines 15-25; Tab. I-1</p> <p style="text-align: center;">-----</p>	1-11

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC1/US 95/13899

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9808771	09-08-98	AU-B- 647732	31-03-94
		AU-B- 5849690	24-08-90
		AU-B- 6598694	08-09-94
		CA-A- 2838398	16-09-92
		EP-A- 0555205	18-08-93
		JP-T- 4504415	06-08-92
		LT-A.8 667	31-01-95
		LV-B- 10284	20-04-95
